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	ates/sec
OM nucleic - nucleic search, using sw model	April 30, 2004, 14:44:42 ; Search time 3927 Seconds (without alignments) 9966.580 Million cell updates/sec
OM nucleic	Run on:

	9966.580 MILLION CELL UPDATES/BEC
Title: Perfect score: Sequence:	US-10-202-687-1 903 1 atggacctgccccgcagctggggcaagtcccagaagtaa 903
Scoring table: IDENTITY_NUC Gapop 10.0,	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues

6940544 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em\_vi:\*
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1. gb\_ba:\*

3. gb\_hrg;\*

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Pred. No. is the number of results predicted by chance to have a em\_htgo\_mus:\* em\_htgo\_other:\*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score   Autch Langth DB   ID   Description	Score Query  Match Length DB ID  MAC19189  903 100: 0 903 6 AK49189  903 100: 0 903 6 AK29181  903 10: 0 AR01871  903 10: 0 AR01871  903 10: AR01871  904 10: B11 10: AR01871  905 10: AR01871  905 10: AR01871  906 10: AR01871  907 10: AR01871  908 66. 2 238725  908 66. 2 238725  909 10: AR018724  900 10: AR01872  900 10:	Score Query  Match Length DB ID  MACA9189  903 100:0  903 6 AK49189  AK475043 AK49189  AK475043 AK49189  AK475043 AK476874  903 100:0  903 100:0  903 6 AK475043  AK775045 AK476871  AK908741 AK108751  AK908774 AK476871 AK108771  AK908774 AK476871 AK108771  AK908774 AK4788  604.4 66.9  903 10 AB095746  604.4 66.9  903 10 AB095746  AK775045 AK108771  AK108774 AK108771  AK108774 AK108 mus  AK108774 AK108771  AK108774 AK108774  AK108774 AK108774  AK108774 AK108774  AK108774 AK108774  AK108774 AK108774  AK108774 AK10877  AK108774 AK10877  AK108774 AK1087  AK10877 AK1087  AK10877 AK1087  AK1087 AK1087			æ				٠
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18         582         64.5         154673         2         AC079472         AC070472	18       582       64.5       154673       2       AC079472       AC079472       AC079472       MC079472       MC0704747       MC070474       MC07	18         582         64.5         154673         2         AC079472         AC079472         AC079472         MAC05474         MAC05474         AC146547         AC166555         AC1665	17	288				AC126062	Rattus
19         134.6         14.9         207989         2         AC146547         AC146647         AC146647         AC146664         AC146666         AC14666         AC14666<	19 134.6 14.9 207989 2 AC146547 AC146547 AC146547 Gaster 21 13.4 13.7 1841 6 AR140519 AR140519 EA1325 CDNA CI 123.4 13.7 1841 6 E41325 AR308737 AR308737 Seque 22 121.8 13.5 1041 6 AX224754 Seque 22 121.8 13.5 1041 6 AX244756 AX244756 AX24475 Seque 22 121.8 13.5 1061 9 AF024689 AF024689 HOMO AF02689 HOMO AF026899 HOMO AF02689 HOMO AF0289 HOMO AF0289 HOMO AF0289 HOMO AF0289 HOMO AF0289 HOMO AF0	19     134.6     14.9     207989     2     AC146547     AC146547     AC146547     AC146547     Gaste       20     123.4     13.7     1841     6     B41325     B41365     B4136		S	•			AC079472	
20         123.4         13.7         1841         6         AR140519         AR140519         AR140519         AR140519         AR140519         AR140519         AR140519         AR140519         AR1506173         AR22475         AR22475         AR23475         Seque         AR234269         AR23475         Seque         AR234269         AR234269         AR234269         AR234269         AR234269         AR234269         AR234269         AR234269         AR234269         AR2342	20 123.4 13.7 1841 6 AR140519 AR140519 AR140519 Seque 21 123.4 13.7 1841 6 E 841325 B41325 CDNA CJ 22 121.8 13.5 1041 6 AR224754 AX224754 Seque 22 121.8 13.5 1041 6 AX224754 AX224754 Seque 22 121.8 13.5 1041 6 AX224756 AX224756 AX224756 Seque 22 121.8 13.5 1041 6 AX224756 AX224756 AX224756 Seque 22 121.8 13.5 1041 6 AX549319 AF024689 AF024689 Homo 28 121.8 13.5 1061 9 AF024689 AF024689 Homo 29 121.8 13.5 1061 9 AF024689 AF024689 Homo 20 18.6 13.1 1041 6 AR30752 AX318795 AF002551 Homo 20 18.6 9.4 1534 6 BD137966 AF024689 Homo 20 18.6 9.4 4895 6 AR224400 AR223400 AR223400 Seque 20 18.6 9.4 4895 6 AX211769 A	20     123.4     13.7     1841     6     AR140519     AR140519     AR140519     AR140519     AR140519     AR140519     AR140519     AR140519     AR140519     AR1640519     AR1640519     AR1640519     AR1640519     AR1640519     AR1640519     AR1640519     AR1640519     AR1640519     AR264754     AR26475     AR26475     AR26475     AR26475     AR26475     AR26475     Seque     AR26475     Seque     AR26475     Seque     AR26475     Seque     AR26475     Seque     AR26489     AR264989     AR	19	134				AC146547	Gasteros
21     123.4     13.7     1841     6     R41325     R41325     CDNA CJ       22     121.8     13.5     1041     6     AX224754     AX224756     AX224756     Seque       24     121.8     13.5     1041     6     AX224756     Seque       25     121.8     13.5     1041     6     AX224756     Seque       26     121.8     13.5     1061     9     AF024689     AX224756     Seque       26     121.8     13.5     1061     9     AF024689     AF024689     HWD024689     HWD0025557     HWD0025557     HWD002557     HWD002557     HWD002557     HWD002557     HWD002557     HWD002557     HWD00257	21     123.4     13.7     1841     6     R41325     R41325     CDNA CJ       22     121.8     13.5     1041     6     AX224754     AX224756     AX224756     Seque       24     121.8     13.5     1041     6     AX224756     AX224756     Seque       25     121.8     13.5     1041     6     AX224756     Seque       26     121.8     13.5     1061     9     AF024689     AX224756     Seque       27     121.8     13.5     1061     9     AF024689     AX22476     Seque       28     121.8     13.5     1061     9     AF024689     AX22476     Seque       29     121.8     13.5     1061     9     AF024689     AF024689     HOMO       29     121.8     13.5     1041     6     AX308752     AX308752     AX308752     AX308752     AX308752     AX308752     AX431102     AX43102     AX431102     AX43102     AX400214     AX4000214     AX4000214     AX4000214     AX4000214     AX4000214	21     123.4     13.7     1841     6     R41325     B41325     CDNA CJ       22     121.8     13.5     1041     6     AX224754     AX224756     AX224756     Seque       24     121.8     13.5     1041     6     AX224756     AX224756     Seque       25     121.8     13.5     1041     6     AX224756     AX224756     Seque       26     121.8     13.5     1041     6     AX224756     AX24756     Seque       26     121.8     13.5     1041     6     AX224756     Seque       27     121.8     13.5     1041     6     AX224756     Seque       28     121.8     13.5     1041     6     AX224756     Seque       29     121.8     13.5     1041     6     AX224756     Seque       29     121.8     13.5     1041     6     AX308752     Seque       30     118.6     13.1     1041     6     AX308752     Seque       31     84.6     9.4     1154     9     AX000521     AX000521     Homo       31     84.6     9.4     1154     9     AX242695     AX242106     Seque       32 <td< td=""><td>20</td><td>123</td><td>•</td><td></td><td></td><td>AR140519</td><td></td></td<>	20	123	•			AR140519	
22     121.8     13.5     1041     6     AR224754     AX224754       23     121.8     13.5     1041     6     AX224754     AX224754       24     121.8     13.5     1041     6     AX224754     AX224756       25     121.8     13.5     1041     6     AX224756     AX224756       26     121.8     13.5     1061     9     AY604688     AY6024688     HOMO24688       28     121.8     13.5     1061     9     AY6024689     AY6024688     HOMO24688       29     121.8     13.5     1061     9     AY6024689     AY6024688     HOMO2567       29     121.8     13.5     1061     9     AY603657     HOMO     AY602567       30     118.6     13.1     1041     6     AX603557     HOMO     AY431102       31     84.6     9.4     1158     9     AY431102     AY431102     HOMO       34     84.6     9.4     1534     6     BD137966     BD137966     BD137966       34     84.6     9.4     1534     6     BA7608214     AY608214     AY608214       34     84.6     9.4     4895     6     AX7242695     AX542269	22 121.8 13.5 1041 6 AR204754 AX224754 AX224754 Seque 24 121.8 13.5 1041 6 AX224754 AX224754 AX224755 Seque 25 121.8 13.5 1041 6 AX224754 AX224756 Seque 26 121.8 13.5 1041 6 AX224756 AX54319 Seque 27 121.8 13.5 1061 9 AF024688 AF024688 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO AF024689 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO AF024689 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO AF02511 HOMO 31 18.6 13.1 1041 6 AK308752 AX431102 HOMO 31 84.6 9.4 1153 9 AF03667 HOMO AF02511 HOMO 34 1534 6 BD137966 FOOCE BD13796 FOOCE BD137966 FOOCE BD13796 FOOCE BD13796 FOOCE BD13796 FOOCE BD137966 FOOCE BD13796 F	22     121.8     13.5     1041     6     AR2304754     AR224754     AR224754       23     121.8     13.5     1041     6     AX224754     AX224754     AX224754       24     121.8     13.5     1041     6     AX224754     AX224756     AX224756       25     121.8     13.5     1041     6     AX224756     AX224756     Seque       26     121.8     13.5     1061     9     AY60369     AY604688     AY604688       29     121.8     13.5     1061     9     AY603657     AY604689     AY604688       29     121.8     13.5     1061     9     AY603657     AY604689     AY604689       29     121.8     13.5     1061     9     AY603657     AY606557     AY606557       30     118.6     9.4     1158     9     AY431102     AY606557     AY606557       31     84.6     9.4     11534     9     AY431102     AY431102     AY606514       34     84.6     9.4     1534     9     AY606514     AY606514     AY606514       35     84.6     9.4     14895     6     AR542400     AR542340     AR543230       36     84.6 <td< td=""><td>21</td><td>123.</td><td>•</td><td></td><td></td><td>E41325</td><td>E41325 cDNA clone</td></td<>	21	123.	•			E41325	E41325 cDNA clone
23     121.8     13.5     1041     6     AX224754     AX224754     Seque       24     121.8     13.5     1041     6     AX224756     AX224756     AX224756     Seque       25     121.8     13.5     1041     6     AX524319     AX524319     AX5244756     Seque       26     121.8     13.5     1061     9     AF024689     AF024689     AF024689     HOMO       29     121.8     13.5     1661     9     AF024689     AF024689     AF024689     HOMO       29     121.8     13.5     1661     9     BC035657     BC035657     HOMO       30     118.6     13.1     1041     6     AX308752     BC035657     AX431102     HOMO       31     84.6     9.4     1158     9     AY600214     AX600214     AX600214     AX6000214     AX6	23 121.8 13.5 1041 6 AX224754 AX224754 Seque 22 121.8 13.5 1041 6 AX224756 AX224756 GAZ24756 Seque 22 121.8 13.5 1041 6 AX224756 AX224756 GAZ24756 Seque 22 121.8 13.5 1041 6 AX524319 AXC244756 AXC244756 AXC244756 Seque 22 121.8 13.5 1061 9 AF024689 AF024689 Homo 28 121.8 13.5 1061 9 AF024689 AF024689 Homo 29 121.8 13.5 1061 9 AF024689 AF024689 Homo 29 121.8 13.5 1041 6 AX308752 AXC002511 Humar 30 118.6 13.1 1041 6 AX308752 AXC002511 Humar 31 84.6 9.4 11534 6 BD137966 BD137966 BD137966 BC00251 Homo 34 84.6 9.4 1534 6 BD137966 BD137966 BC00251 Homo 35 84.6 9.4 4895 6 AXC242400 AXC242695 Seque 36 84.6 9.4 4895 6 AXC21400 AXC242695 Seque 37 84.6 9.4 4895 6 AXC21400 AXC242695 Seque 38 84.6 9.4 4895 6 AXC214769 AXC00873 Homo 39 84.6 9.4 11828 9 AF038419 AXC00873 Homo 39 84.6 9.4 121886 2 BX663530 BX663529 Gallu 4 83.4 9.2 84653 2 BX663529 BX663529 BX663526 Gallu 45 83.4 9.2 254295 2 BX663525 BX663526 Gallu 45 BX663526 Gall	23     121.8     13.5     1041     6     AX224754     AX224754     Seque       24     121.8     13.5     1041     6     AX224756     AX224756     AX224756     AX224756     Seque       25     121.8     13.5     1041     6     AX524319     AX524756     Seque       26     121.8     13.5     1061     9     AF024689     AF024689     HOMO       29     121.8     13.5     1661     9     AF024689     HOMO     AF024689     HOMO       29     121.8     13.5     1661     9     AF024689     HOMO     AF024689     HOMO       29     121.8     13.5     1661     9     AF024689     HOMO     AF0024689     HOMO       29     121.8     13.5     1661     9     AF002511     HOMO     AF002551     HOMO       30     18.6     9.4     1158     9     AF0002511     HOMO     AF03016214     AF0002511     HOMO       31     84.6     9.4     14895     6     AR234400     AR223400     AR223400     Seque       32     84.6     9.4     4895     6     AK234200     AK24239     AK24239     AK24239       38     84.6     <	22	121.				AR308737	_
24     13.5     1041     6     AX224756     AX224756     Seque       25     121.8     13.5     1041     6     AX549319     AX549319     AX549319       26     121.8     13.5     1061     9     AF024689     AF024689     AR024689       27     121.8     13.5     1061     9     AF024689     AR024689     HORO24689       28     121.8     13.5     1061     9     AF024689     AR024689     HORO24689       29     121.8     13.5     1649     9     AR020557     BC035557     HORO25569       30     118.6     13.1     1041     6     AR308752     AR308752     Seque       31     84.6     9.4     1534     9     AC002511     HORO       32     84.6     9.4     1534     9     AF080214     AR108643     AR108643     AR108643     AR108643     AR224695     Seque       34     84.6     9.4     4895     6     AR242400     AR242695     Seque       36     84.6     9.4     4895     6     AR242400     AR242695     Seque       37     84.6     9.4     4895     6     AR242409     AR242695     AR242695     Seque	24     121.8     13.5     1041     6     AX224756     AX224756     SAGUE       25     121.8     13.5     1041     6     AX549319     AX549319     AX549319       26     121.8     13.5     1061     9     AF024689     AX549319     AX549319       27     121.8     13.5     1061     9     AF024689     AX5024689     AX6024689     HOMO24689       28     121.8     13.5     1654     9     BC035557     BC035557     HOMO       29     121.8     13.1     1041     6     AX308752     AX508752     Seque       31     184.6     9.4     1534     9     AC002511     HOMO       34     84.6     9.4     1534     9     AY690214     AX108752     Seque       34     84.6     9.4     1534     9     AY690214     AX108754     AX1080214       34     84.6     9.4     1534     9     AX2142695     AX108754     AX108754       36     84.6     9.4     4895     6     AX2142695     AX22430     AX22430       37     84.6     9.4     4895     6     AX211769     AX211769       40     84.6     9.4     4895     6<	24     13.5     1041     6     AX224756     AX224756     SAGURE       25     121.8     13.5     1041     6     AX549319     AX549319     AX549319       26     121.8     13.5     1061     9     AF024689     AF024689     AF024689       27     121.8     13.5     1061     9     AF024689     AF024689     HOMO       29     121.8     13.5     1694     9     BC025557     BC035657     HOMO       29     121.8     13.1     1041     6     AR306752     BC035657     HOMO       31     84.6     9.4     1154     9     AC002511     HOMO       32     84.6     9.4     1154     9     AK7080214     HOMO       34     84.6     9.4     1534     6     AR22430     AR23102     AR23102     AR23102       36     84.6     9.4     4895     6     AR242695     AR22430     AR224269     Seque       37     84.6     9.4     4895     6     AR242695     AR242469     AR242409     AR26350     Seque       38     84.6     9.4     4895     6     AR242695     AR242469     AR264269     AR264269     AR264269       3	23	121.	13.5			AX224754	
25         13.5         1041         6 AX549319         AX549319         AX549319         AX549319         AX549319         AX549319         AX549319         AX549319         AY54319         AY54319         AY54688         AY54688         AY54688         AY5024689         AY6024689         AY6024689         AY6024689         AY602557         AY6002557         AY6002551         AY6002511         AY600214         AY60021	25 121.8 13.5 1041 6 AX549319 AX549319 AX549319 AX549319 BXC02511 HVD0 27 121.8 13.5 1061 9 AF024688 AF024688 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO 27 121.8 13.5 1061 9 AF024689 HOMO 28 121.8 13.5 1061 9 AF024689 HOMO 29 121.8 13.5 1061 9 AF024689 HOMO 29 121.8 13.5 1064 9 AF020557 HOMO 29 121.8 13.5 1064 9 AX931102 HOMO 29 11.8 9 AY431102 HOMO 29 11.8 9 AY431102 HOMO 29 4 1534 6 BD137966 FOCK BROOK BROO	25         121.8         13.5         1041         6         AX549319         AX545829         AX54588         AX54589         AX54589 <t< td=""><td>24</td><td>121.</td><td>13.5</td><td></td><td></td><td>AX224756</td><td></td></t<>	24	121.	13.5			AX224756	
26         121.8         13.5         1061         9         AF024688         AF024688         HOMO           27         121.8         13.5         1061         9         AF024689         AF023651         HUMB         AF023651         HUMB         AF023651         AF023651         AF023162         AF023162         AF023162         AF023162         AF078021         HUMB         AF078021         HUMB         AF08021         AF078021         HUMB         AF078021         AF078021         HUMB         AF078021         AF078021         HUMB         AF078021         AF078021         AF078021         AF078021         AF078021         AF078021         AF0780021         AF07800021         AF0780021         AF0780002	26 121.8 13.5 1061 9 AF024688 AF024688 Homo 27 121.8 13.5 1061 9 AF024689 PROME AF024689 Homo 28 121.8 13.5 1661 9 AF024689 PROME AF024689 Homo 28 121.8 13.5 1694 9 BC035657 AC002511 Human 29 121.8 13.5 1694 9 BC035657 AC002511 Human 29 118.6 13.1 1041 6 AF23657 AC002511 Human 29 44.6 9.4 11584 9 AY431102 AY431102 AY431102 Homo 29 44.6 9.4 1534 6 BD137966 Profe AF080214 Homo AF	26         12.18         13.5         1061         9         AF024688         AF024689         PO024689         HOMO24689         HOMO2511         HOMO26814         HOMO26814         HOMO2714         HOMO27	25	121.	13.5	_	9	AX549319	Segue
27         121.8         13.5         1061         9         AF024689         AF024689         AF024689         HOMO           28         121.8         13.5         1694         9         BC035657         BC035657         HOMO           29         121.8         13.5         98713         9         AC002511         AR308752         AR308752         AR431102         AR431102 </td <td>27         121.8         13.5         1061         9 AF024689         AF024689         AF024689         HOMO24689         HOMO2689         AF024689         HOMO229         28         121.8         13.5         1694         9 BC035657         BC035657         HOMO2569         HOMO259         AF0002511         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HUMO25657         HUMO25657         HUMO256567         HUMO25667         HUMO25667         AF0002514         HUMO256         HUMO25</td> <td>27         121.8         13.5         1061         9         AF024689         AF024689         HOMO           28         121.8         13.5         1694         9         BC035657         BC035657         HOMO           29         121.8         13.5         1694         9         AC002511         AC002511         HOMO           30         118.6         13.1         1041         6         AR308752         AC002511         HUMO           31         84.6         9.4         1534         9         AC00214         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC000214         AC000214         AC00214         AC000214         AC00021</td> <td>26</td> <td>121.</td> <td>13.5</td> <td>_</td> <td>σ</td> <td>AF024688</td> <td>Homo</td>	27         121.8         13.5         1061         9 AF024689         AF024689         AF024689         HOMO24689         HOMO2689         AF024689         HOMO229         28         121.8         13.5         1694         9 BC035657         BC035657         HOMO2569         HOMO259         AF0002511         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HOMO25657         HUMO25657         HUMO25657         HUMO256567         HUMO25667         HUMO25667         AF0002514         HUMO256         HUMO25	27         121.8         13.5         1061         9         AF024689         AF024689         HOMO           28         121.8         13.5         1694         9         BC035657         BC035657         HOMO           29         121.8         13.5         1694         9         AC002511         AC002511         HOMO           30         118.6         13.1         1041         6         AR308752         AC002511         HUMO           31         84.6         9.4         1534         9         AC00214         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC002514         AC000214         AC000214         AC00214         AC000214         AC00021	26	121.	13.5	_	σ	AF024688	Homo
28     121.8     13.5     1694     9     BC035657     BC035657     HOMOS511       29     121.8     13.5     98713     9     AC002511     AC002511     HUMBAR       30     118.6     13.1     104.1     6     AR308752     AX431102     AX308752     AX431102     AW308752       31     84.6     9.4     1534     6     BD137966     BD137966     BD13796     PFOCE       33     84.6     9.4     1534     6     BD137966     BD13796     PFOCE       34     84.6     9.4     1534     6     BR108643     AR108643     AR108643     AR108643     AR223400     AR223400     Seque       35     84.6     9.4     4895     6     AR242695     AR223400     AR223400     Seque       37     84.6     9.4     4895     6     AX542290     AX543230     AX543230     AX543230     AX541769       40     84.6     9.4     4925     6     AX211769     AR211769     AR211769       41     84.6     9.4     11828     9     AR545851     AR541769       41     84.6     9.4     11828     9     AR5653530     AR563530     BX663529     Gallu       42	28 121.8 13.5 1694 9 BC035657 BC035657 HOMO 2511 HUMBER 25 121.8 13.5 9 AC002511 AC002511 HUMBER 25 121.8 13.5 98713 9 AC002511 HUMBER 25 SEQUENCE 25 SEX	28 121.8 13.5 1694 9 BC035657 BC035657 HOMD 22 121.8 13.5 1694 9 BC035657 HOMD 22 121.8 13.5 98113 9 AC00511 AC00511 HUMBER 22 121.8 13.5 98113 9 AC00511 AC00511 HUMBER 23 184.6 9.4 1158 9 AY431102 HOMD 23 84.6 9.4 1534 6 BD137966 BC052 BC0	27	121	13.5	-	0	AF024689	Homo
29 121.8 AC002511 Human AC002511 Human 313.5 98713 9 AC002511 Human 313.6 98713 9 AC002511 Human 313.6 91.1 1041 6 AK308752 AX431102 AX431102 BOD33766 Force 314.6 9.4 11534 9 AY431102 AX431102 HOMO 314 84.6 9.4 1534 6 BD137966 Force 315 84.6 9.4 4895 6 AR108643 AR22400 AR22400 AR22400 AX223400 Seque 317 84.6 9.4 4895 6 AX242695 AX549230 Seque 3184.6 9.4 4895 6 AX242695 AX549230 Seque 40 84.6 9.4 4225 6 AX211769 AX	29 121.8 J. 98713 9 AC002511 AC002511 Human 30 118.6 J. 1141 6 AR308752 AX308752 AX308752 Seque 31 84.6 9.4 1158 9 AX431102 AX431102 Homo 32 84.6 9.4 11534 9 AX431102 AX431102 Homo 33 84.6 9.4 1534 9 AX431102 AX431102 Homo 34 84.6 9.4 4895 6 AR20340 AR20340 Seque 35 84.6 9.4 4895 6 AR20340 AX20340 Seque 36 84.6 9.4 4895 6 AX52340 AX542695 AX542695 AX542695 Seque 37 84.6 9.4 4895 6 AX52340 AX542695 Seque 38 84.6 9.4 4895 6 AX5421769 AX542695 Seque 38 84.6 9.4 4895 9 AX5421769 AX542695 Seque 40 84.6 9.4 11828 9 AX5421769 A	29 121.8 13.5 98713 9 AC002511 Human 2002511 Human 31 18.6 13.1 1041 6 AC002511 AC002511 AC002511 Human 32 118.6 13.1 1141 6 9.4 1158 9 AY431102 AX431102 BD137966 Protes 32 84.6 9.4 1534 9 AY431102 AC00214 Homo 33 84.6 9.4 4895 6 AR20340 AR20340 AR20340 AR20340 Seque 34.6 9.4 4895 6 AR20340 AR20340 AR20340 Seque 35 84.6 9.4 4895 6 AR20340 AR20340 AR20340 Seque 36 84.6 9.4 4895 6 AR20340	28	121	13.5		σ.	BC035657	Ношо
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31 84.6 9.4 1158 9 AY431102 AY431102 HOMO 32 84.6 9.4 1534 9 BD137966 BD137966 Prote 84.6 9.4 1534 9 AF080214 AF080214 AR108643 Seque 84.6 9.4 4895 6 AR233400 AR233400 Seque 84.6 9.4 4895 6 AR233400 AR233400 Seque 84.6 9.4 4895 6 AX542930 Seque 98.6 9.4 4895 6 AX542930 Seque 98.6 9.4 4895 6 AX542930 AX549230 Seque 40.8 84.6 9.4 4895 6 AX54930 AX549330 Seque 40.8 84.6 9.4 11228 9 AF055917 AX211769 AX211769 Seque 40.8 84.6 9.4 11288 9 AF34819 BX663520 AX3411769 AX211769 AX3411769 AX211769 AX3411769 AX211769 AX3411769 AX211769 AX3411769 AX211769 AX3411769 AX34117769 AX3411769 AX34117769 AX3411769 AX341	31 84.6 9.4 1158 9 AY431102 AY431102 HOMO 32 84.6 9.4 1534 9 BD137966 BD137966 Prote 84.6 9.4 1534 9 AF080214 BD137966 BD137966 Prote 84.6 9.4 1534 9 AF080214 AR080214 HOMO 34 84.6 9.4 4895 6 AR23400 AR223400 Seque 84.6 9.4 4895 6 AX542340 AX542505 Seque 94.6 9.4 4895 6 AX542591 AX542505 Seque 94.6 9.4 4895 9 AF055917 AX542510 Seque 94.6 9.4 4895 9 AF055917 AX211769 Seque 94.6 9.4 11828 9 AF34819 BX653510 BX653510 BX653510 BX653510 BX653510 BX653510 BX653510 BX653520 Gallu 42 84.4 9.3 131743 2 BX653529 BX653529 Gallu 42 84.4 9.3 131743 2 BX653529 BX653529 Gallu 44 83.4 9.2 254295 2 BX653526 BX653526 Gallu 45 83.4 9.2 254295 2 BX653526 BX653526 Gallu 45	31 84.6 9.4 1158 9 AY411102 AY4311102 HOMO 32 84.6 9.4 1534 6 BD137966 BD137966 Prote 8 33 84.6 9.4 1534 6 BD137966 BD137966 Prote 8 34 84.6 9.4 4895 6 AR203400 AR223400 Seque 8 35 84.6 9.4 4895 6 AR242695 AX549230 Seque 8 37 84.6 9.4 4895 6 AX549230 AX549230 Seque 9 38 84.6 9.4 4895 9 AY51769 AX549230 Seque 6 40 84.6 9.4 1288 9 AY5384819 AX549230 Seque 9 41 84.6 9.4 12188 2 BX663530 BX663530 GA1104 AX549230 Seque 9 42 84.6 9.4 24281 9 AX5384819 AX549230 GA1104 AX549230 Seque 9 43 84.4 9.3 131743 2 BX663529 BX663329 GA1104 AX54923 Seque 9 44 9.3 131743 2 BX663529 BX663529 GA1104 AX54929 Seque 9 45 83.4 9.2 254295 2 BX663529 GA1104 AX54929 Seque 9 45 83.4 9.2 254295 2 BX663526 GA1104 AX54929 Seque 9 45 83.4 9.2 254295 C BX663526 GA1104 AX54929 C BX663528 GA1104 AX54929 C BX663528 GA1104 AX54929 C BX663528 GA1104 AX54929 C BX663528 GA1104 C BX663528 GA1104 C BX663528 GA1104 C BX663528 GA1104 C BX663528	30	118	13.1		ø	AR308752	
32 84.6 9.4 1534 6 BD137966 BD137966 PCCCE 33 84.6 9.4 1534 9 AF080214 AF080214 HOMO 34 84.6 9.4 4895 6 AR233400 AR233400 Seque 35 84.6 9.4 4895 6 AR233400 AR234595 AR242695 Seque 36 84.6 9.4 4895 6 AR23340 AR242695 Seque 38 84.6 9.4 4895 9 AF085917 AR242695 Seque 39 84.6 9.4 4895 9 AF085917 AR243691 AF34819	32 84.6 9.4 1534 6 BD137966 BD137966 PCCE 33 84.6 9.4 1534 9 AF080214 AF080214 HOMO 34 84.6 9.4 4895 6 AR23400 AR223400 Seque 35 84.6 9.4 4895 6 AR23400 AR242695 Seque 36 84.6 9.4 4895 6 AR22340 AR242695 Seque 38 84.6 9.4 4895 9 AF085917 AR242695 Seque 39 84.6 9.4 4895 9 AF085917 AR242695 Seque 40 84.6 9.4 11288 9 AF384819 AF384819 AF384819 HOMO 41 84.6 9.4 121886 2 BX663530 BX663530 GAILU 42 84.6 9.4 248281 9 AC008737 AC008737 HOMO 43 84.4 9.2 131343 2 BX663529 BX663529 GAILU 45 83.4 9.2 254295 2 BX663526 BX663526 GAILU 45 83.4 9.2 254295 2 BX663526 BX663526 GAILU	32     84.6     9.4     1534     6     BD137966     BD137966     BD137966     BD137966     BD137966     BD137966     BD137966     PACCORD14     ARCORD14     HOME     ARCORD14     ARCORD14     ARCORD14     ARCORD14     ARCORD14     HOME     ARCORD14     ARCORD14     ARCORD14     ARCORD14     ARCORD14     ARCORD14     ARCORD17     ARCORD17     HOME       41     81.4     9.2     244281     2     ARCORD13     ARCORD17     ARCORD1	31	84	9.4		σ	AY431102	
33         84.6         9.4         1534         9 AF080614         AF0800214 Homo           34         84.6         9.4         4895         6 AR108643         AR108643         AR108643           35         64.6         9.4         4895         6 AR224400         AR224595         AR242695           37         84.6         9.4         4895         6 AR242695         AR242695         AR242695         AR242695         Seque           38         84.6         9.4         4995         6 AR242695         AR242695         Seque           39         84.6         9.4         4995         6 AR242693         Seque         AR211769         Seque           40         84.6         9.4         4925         6 AR211769         AR211769         Seque           40         84.6         9.4         112186         2 AR534819         AR784819         Homo           41         84.6         9.4         12186         2 AR534819         AR564310         AR564319         AR564319         AR5663130         AR5663130         AR566311           44         83.4         9.2         248281         2 AR563523         AR546323         AR563526         Gallu           44	33 84.6 9.4 1534 9 AF080214 AF080214 Homo and a sequence of the control of the co	33 84.6 9.4 1534 9 AF080214 AF080214 Homo and a 84.6 9.4 4995 6 AR108643 AR22469 Seque a 84.6 9.4 4895 6 AR22340 AR224269 Seque a 84.6 9.4 4895 9 AF085917 AR211769 AR24269 Seque a 84.6 9.4 4895 9 AF085917 AR211769 AR2117	32	84.	9.4	1534	9	BD137966	Prote
34         84.6         9.4         4895         6         AR108643         AR108643         AR108643         AR108643         AR2108643         Seque         36         44.6         9.4         4895         6         AR223400         AR223400         Seque         AR223400         Seque         37         84.6         9.4         4895         6         AR242695         AR242695         Seque         AR242695         Seque         AR242695         Seque         AR242695         Seque         AR242695         Seque         AR242695         Seque         AR2495917         AR24950         AR211769         AR211769         AR211769         AR211769         AR211769         AR211769         AR211769         AR344819	34 84.6 9.4 4895 6 AR108643 AR108643 Seque 364.6 9.4 4895 6 AR223400 AR223400 Seque 36 84.6 9.4 4895 6 AR223400 AR223400 Seque 37 84.6 9.4 4895 6 AR242695 AX549230 AX549230 Seque 38 84.6 9.4 4895 9 AF055917 AF059230 Seque 40 84.6 9.4 11228 9 AF34819 AX211769 AX211769 Seque 41 84.6 9.4 11228 9 AF34819 AX211769 AX211769 Seque 42 84.6 9.4 11288 9 AF34819 BX663530 BX663530 AX211769	34 84.6 9.4 4895 6 AR108643 AR108643 Seque 36 84.6 9.4 4895 6 AR223400 AR223400 Seque 36 84.6 9.4 4895 6 AR243695 AX549230 Seque 37 84.6 9.4 4895 6 AR243695 AX549230 Seque 38 84.6 9.4 4895 9 AK549230 Seque 40 84.6 9.4 4225 6 AX211769 AX211769 AX211769 Seque 40 84.6 9.4 12188 9 AR384819 AX211769 AR284819 Homo 41 84.6 9.4 12188 2 BX663530 BX663530 BX663530 GAIlu 44 9.3 131143 2 BX663529 GAIlu 44 9.2 254295 2 BX663526 GAIlu 45 83.4 9.2 254295 2 BX663526 GAIlu 45 ALIGNMENTS	33	84.		1534	0	AF080214	Ношо
35	35	35	34	84.		4895	9	AR108643	_
36 84.6 9.4 4895 6 AR242695 AR242695 Seque 37 84.6 9.4 4895 6 AX549230 AX549230 Seque 38 84.6 9.4 4895 6 AX549230 AX549230 Seque 38 84.6 9.4 4895 6 AX211769 AX211769 Seque 40 84.6 9.4 11828 AX211769 AX211769 Seque 41 84.6 9.4 121886 2 BX663530 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AXC008737 AXC008737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 BX663526 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 BX663526 G	36 84.6 9.4 4895 6 AR242695 AR242695 Seque  37 84.6 9.4 4895 6 AX549230 AX549230 AX549230 Seque  38 84.6 9.4 4895 6 AX211769 AX211769 Seque  40 84.6 9.4 11828 9 AF534819 AF34819 AF34819 Homo  41 84.6 9.4 121886 2 BX635330 BX653330 Gallu  42 84.6 9.4 248281 9 AC008737 AC008737 Homo  43 84.4 9.3 131743 2 BX653529 BX663529 Gallu  44 83.4 9.2 254295 2 BX653526 BX663526 Gallu  45 83.4 9.2 254295 2 BX653526 BX663526 Gallu  45 83.4 9.2 254295 2 BX663526 BX663526 Gallu  46 83.4 9.2 254295 2 BX663526 BX663526 Gallu  47 83.4 9.2 254295 2 BX663526 BX663526 Gallu	36 84.6 9.4 4895 6 AK5242695 AR242695 Seques 84.6 9.4 4895 6 AK5242695 Seques 84.6 9.4 4895 6 AK529330 AK5243230 Seques 84.6 9.4 4895 6 AK5213769 Seques 84.6 9.4 1828 9 AF055917 AK211769 Seques 41 84.6 9.4 121868 2 AK534819 AK534819 AK63530 GAILU 42 84.6 9.4 121868 2 BK663539 BK663530 GAILU 43 84.4 9.2 131743 2 BK663529 BK663529 GAILU 45 83.4 9.2 254295 2 BK663526 GAILU 45 BAILU 49.2 254295 2 BK663526 GAILU 45 BAILU 45 BAILU 45 BAILU 45 BAILU 45 BAILU AK63526 GAILU AK6356 BAILU AK63526 GAILU AK6356 BAILU AK63526 GAILU AK6356 BAILU AK636 BAILU AK648 BAILU A	35	<b>84</b> .		4895	9	AR223400	_
37         84.6         9.4         4895         6 AX559230         AX549230 Seque           38         84.6         9.4         4895         9 AF055917         AF055917 HOMO           39         84.6         9.4         11828         6 AX211769         AX211769           40         84.6         9.4         11828         9 AF384819         AK2817769           41         84.6         9.4         21886         2 RX665330         BX663530         BX663530           43         84.4         9.4         248281         9 AC008737         AC008737         AC008737         BX663529         Gallu           44         83.4         9.2         846352         2 BX663523         BX663523         Gallu           45         83.4         9.2         254295         2 BX663523         BX663526         Gallu	37 84.6 9.4 4895 6 AX559230 AX559230 Seque 84.6 9.4 4895 9 AP055917 AP050208 Seque 40 9.4 4225 6 AX211769 BX663530 BX663530 BX663530 BX663530 AX211769 AX21769 AX21769 AX21769 AX21769	37 84.6 9.4 4895 6 AX5.9230 AX5.9230 Seque 84.6 9.4 4895 9 AY6.55917 APOS.5917 APOS.59	36	84.		4895	9	AR242695	
38         84.6         9.4         4895         9         AF055917         HOMDO           39         84.6         9.4         4925         6         AF211769         Seque           40         84.6         9.4         11828         9         AF384819         AF384819         AF384819         HOMDO           42         84.6         9.4         121886         2         BK663530         Gallu           43         84.6         9.4         248281         9         AC008737         HOMDO           43         84.4         9.3         131743         2         BK663529         BX663529         BX663529           44         83.4         9.2         254295         2         BX663526         Gallu           45         83.4         9.2         254295         2         BX663526         Gallu	38 84.6 9.4 4895 9 AF055917 AF055517 Homo 39 84.6 9.4 4825 6 AX211769 AX211769 Seque 41 84.6 9.4 11828 9 AF34819 AF384919 Homo 42 84.6 9.4 121886 2 BX663530 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC08737 AC08737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 BX663529 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 BX	38 84.6 9.4 4995 9 AF055917 AF055517 Homood March 196 9.4 4925 6 AF211769 AF211769 AF211769 AF211769 AF384819 AF384819 AF384819 Homood March 196 9.4 11828 9 AF384819 AF38481 AF384819 AF384819 AF384819 AF384819 AF384819	37	84.		4895	φ	AX549230	_
39         84.6         9.4         4925         6         AX211769         AX211769         Seque           40         84.6         9.4         11828         9         AF384819         AF384919         AF38663317         AF384819         AF384919         AF384919         AF384919         AF384919         AF3863329         AF384919         AF3863329         AF384919         AF384919         AF3863326         AF384919         AF384919         AF384919         AF3863326         AF384919         AF384919 <t< td=""><td>39 84.6 9.4 4925 6 AX211769 AX211769 Seque 40 84.6 9.4 11828 9 AX28419 AX284819 AX28</td><td>39 84.6 9.4 4925 6 AX211769 AX211769 Seque 40 84.6 9.4 11828 9 AX24819 AX384819 AX384819 AX384819 AX384819 AX384819 AX384819 AX384819 AX8663530 BX663530 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC0009737 AC0009737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 BX</td><td>38</td><td>84.</td><td>9.4</td><td>4895</td><td>σ</td><td>AF055917</td><td>5917</td></t<>	39 84.6 9.4 4925 6 AX211769 AX211769 Seque 40 84.6 9.4 11828 9 AX28419 AX284819 AX28	39 84.6 9.4 4925 6 AX211769 AX211769 Seque 40 84.6 9.4 11828 9 AX24819 AX384819 AX384819 AX384819 AX384819 AX384819 AX384819 AX384819 AX8663530 BX663530 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC0009737 AC0009737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 BX	38	84.	9.4	4895	σ	AF055917	5917
40         84.6         9.4         11828         9         AF384819         AF384819         HOMO           41         84.6         9.4         121886         2         BX665330         BX665350         BX663530         BX663530         BX663530         AC008737         AC008737         AC008737         HC008737         BX663529         Gallu           43         84.4         9.3         131743         2         BX663529         Gallu           44         83.4         9.2         84633         2         BX663523         Gallu           45         83.4         9.2         254295         2         BX663526         Gallu	40 84.6 9.4 11828 9 AF384819 AF384819 HOWO 41 B4.6 9.4 121886 2 BX665330 BX663530 BX663530 GALIAU 42 84.6 9.4 28281 9 AC008737 AC008737 HOWO 43 84.4 9.3 131743 2 BX663529 BX663529 GALIA 44 83.4 9.2 254295 2 BX663523 BX663526 GALIA 45 83.4 9.2 254295 2 BX663526 BX663526 GALIAU	40 84.6 9.4 11828 9 AF384819 AF384819 HOMO 41 B4.6 9.4 121886 2 BX665530 BX665530 BX665530 BX665530 BX665530 BX665530 BX665530 BX665529 Gallu 42 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 254295 2 BX663526 BX663526 Gallu 45 B3.4 9.2 254295 2 BX663526 BX663526 Gallu ALGNWENTS	39	84.	٠.	4925	9	AX211769	1769
41 84.6 9.4 121886 2 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC008737 AC008737 AC008737 Gallu 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 84653 2 BX663523 BX663523 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu	41 84.6 9.4 121886 2 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC008737 AC008737 Homo 43 84.4 9.2 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 84653 2 BX663523 BX663523 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu	41 84.6 9.4 121886 2 BX663530 BX663530 Gallu 42 84.6 9.4 248281 9 AC00877 AC00877 HOMO 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 93.4 9.2 84653 2 BX663526 BX663526 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu ALIGNMENTS	40	84.	9.4		σ	AF384819	1819 Homo
42 84.6 9.4 248281 9 AC008737 AC008737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 84653 2 BX663523 BX663523 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu	42 84.6 9.4 248281 9 AC008737 AC008737 Homo 43 84.4 9.3 131743 2 BX663529 BX663529 BX663529 GALlu 44 83.4 9.2 84653 2 BX663523 BX663523 GALlu 45 83.4 9.2 254295 2 BX663526 BX663526 GALlu Alifonments	42 84.6 9.4 248281 9 AC008737 AC008737 HOMO 43 84.4 9.3 131743 2 BX663529 BX663529 Gallu 44 83.4 9.2 24295 2 BX663526 BX663526 Gallu 45 83.4 9.2 254295 2 BX663526 BX663526 Gallu ALIGNMENTS	41	84	9.4	Н	0	BX663530	3530 Gallus
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Sequence 249 from patent US 6555339. AR308734 GI:31700263 Unknown. RESULT 1
AR308734
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE

PAT 12-JUN-2003

linear

DNA

Unknown.
Unclassified.
I (bases 1 to 903)
Liaw,C.W., Behan,D.P. and Chalmers,D.T.
Non-endogenous, constitutively activated human protein-coupled receptors
Patent: US 6555339-A 249 29-APR-2003;

JOURNAL

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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541 CCGGCCCGCTTCAGCCTTCTCTCTCTCTCTCTCTTTTTTCTGCCCTTGGCCATCACAGCCTTC
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                                                                                                                                                                                                                           Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRe), antibodies thereto, and systems for identifying such antiplenic peptides
Patent: WO 20261087-A 474 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 1.5e-132;
iive 0; Mismatches 0;
                                                      903 bp DNA
Sequence 474 from Patent W002061087.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 903; Conservative
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Best Local Similarity 100.0%; Pred. No. 1.5e-132;
Matches 903; Conservative 0; Mismatches 0; Indels
                            /organism="unknown"
/wol_type="genomic DNA"
Location/Qualifiers
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Db 121 AGCCTGGTCTACGCCCTGAACCTGGCTGCTCCTGCTGCTGCTGTCTCTCTGCCC 180  Qy 181 CTGAAGGCGGTGGAGGCGTTAGCCTCCGGGGCCTGGCCT	Qy         241 GTCTTCGCGGTGGCCACTTCTTCCCACTCTATGCCGGGGGGCTTCCTGGCCGCCTG 300           Db         241 GTCTTCGCGGTGGCCCACTTCTTCCCACTCTATGCCGGGGGGGG	QY         301 AGTGCAGGCCGCTACCTGGGAGCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG 360           1	Qy         361 TGCTAFTCCTGGGGGGTGTGCGCGGCCATCTGGGCCTCGTCTGTGTCACCTGGGTCTG         420           bb         361 TGCTAFTCCTGGGGGGTGTGCGGGCCATCTGGGCCTTGTGTCTCTGTGTCACTGGGTCTG         420	Qy         421 GTCTTTGGGTTTGGAGGCTCCAGGAGGCTGGACCACGACCACACACCTCCCTGGGCATC 480           Db         421 GTCTTTGGGTTTGGAGGCTCCAGGAGGCTGGCTGGACCACACACA	481 AACACACGGTCAACGGCTCTCCGGTCTGCAGGCCTGGGACCCGGCCTCTGCCGGC	CONTROLLE   CONT	Qy         661         Cadaccaccraacracacacacacacaccaccaccaccacaccac		Qy         781 GGGCTCATCACGGGTGCCTGGAGTGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840           Db         781 GGGCTCATCACGGTGCCTGGAGTGTGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840           Qy         841 AGGGGTCTTGAGCTTGAGTGTGTGCCCAGAAGAAGCAAGAAGCAAGTCCCAAAAG	Db 841 AGGGTCCTGGCCTGAAGACGGTGTGTGTGTGTGTGTGTGT	RESULT 4 AF024687 LOCUS DEFINITION Homo sapiens putative G protein-coupled receptor (GPR40) gene,	_	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Entaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Entheria, Dicheria, Dicheria, Domonalia, Domonalia, Dicheria, Dicheria, Danco	CE 1 (bases 1 to 923) RS Sawzdargo, M., George, S.R., Ng. O'Dowd, B.F.	TITLE A cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1 JOURNAL Biochem. Biophys. Res. Commun. 239 (2), 543-547 (1997)
Db         601         TGCTACGTGGCTGCCTCCGGGCACTGGCCCGCTCCGGCCTGACGACGACGAAGCTG         660           Qy         661         CGGGCCCCTGGGTGGCCGGCGCCCTCCTCACGTTGCTTGC	OY 721 AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGCGGAAGCTG 780	QY         781 GGGCTCATCACGGGTGCCTGAGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840           1	OY 841 AGGGTCCTGGCCTGAAGACAGTGTGCGGCAAGAACGCAAGGGGCAAGTCCCAGAAG 900	Oy 901 TAA 903  Db 901 TAA 903	RESULT 3 AX675043 LOCUS DEFINITION Sequence 1 from Patent W002057783. ACCESION AX675043 ACCESSION AX675043 ACCESSION AX675043		CB RS	TITLE Method of screening for gpr40 ligands JOURNAL Patent: WO 02057783-A 1 25-JUL-2002; Glaxo Group Limited (GB); Smithkline Beecham PLC (GB) FEATURES	source 13v3 /organism="Homo sapiens" /forganism="taxon:9606" /db_xref="taxon:9606" 13v3 /note="unnamed protein product"	/protein_id="CADB3804.1" /protein_id="CADB3804.1" /db_xref="G1:2933352" /db_xref="Renyengener-cadB3804" /translation="MOLPOGSCLYVARFALGFPLNVLAIRGATAHARLRLTPSLVY ALNGCSDLLLTVSLPLRAVBALASGAMPLPASLCFPVRAVAHFPLYAGGGFLAALSA GRYLGAAFFLGYQFRRPCYSWGVCAAIWALNLGCHGLVFGEAPGGWLDHSNTSLGI NTPVNGSPVCTRAWDPASAGPRAFSLSILLFFLPLAITAFCYVGCLRALRSGITHRR	KLRAAWVAGGALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSV GYLGRGFGLKTVCAARTQGGKSQK"	Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-132; Matches 903; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1 ATGGACCTGCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCTGCGCTTGGGCTTGGGCTTC 60	dy         61 CCGCTCAACGTCCTGGCCATCCCAGGCCCACGCCCGGCTCCGTTCACCCCT         120           bb         61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCACGCCTCCGTCTCACCCCT         120	TGCCC

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Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J.,
Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
Sequence analysis of a 1 Mb region in human 19913.1
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Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 100.0%; Pred. No. 1.5e-132;
Conservative 0; Mismatches 0;
                                2 (bases 1 to 923)
O'Dowd, B.F.
Direct Submission
Submitted (15-SEP-1997) Department of Toronto, 8 Taddle Creek Rd., Toronto, Location/Qualifiers
                                                                                                                                                               /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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from hyprid UV5HL9-5B, which carries chromosome 19 as its
only human chromosome"
complement(128. .279)
/note="88" similarity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(<6537. 6570,7043. 7420,10532. .10837,12251. .12517,
12664. .12927,15377. .15634,15839. .16102,16198. .16461,
13325. .19421,19547. .19622,20098. .20216,20647. .20731,
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/product="B-cell receptor CD22-B isoform"
join(<6537. .6570,7043. .7420,10532. .10837,15377. .15634,
15839. .16102,16198. .16461,19325. .19421,19547. .19622,
20098. .20216,20647. .20731,21062. .>21193)
                                                                Direct Submission
Submitted (14-NOV-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walmut Creek, CA 94598, USA
On Nov 7, 2002 this sequence version replaced gi:1498644.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 40kb). It is clipped at the overlap with AC002511. The
number of bases overlapped is 6888.
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join(6377. 6570, 7043. 1740, 10532. 10837, 12251. 12517,
12664. 12927, 15377. 15634, 15839. 16102, 16198. 16461,
19325. 19421, 19547. 19622, 20098. 20216, 20647. 20731,
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                     6 (bases 1 to 34791)
DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="alternatively spliced; B-lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="B-cell receptor CD22-B isoform"
Walnut Creek, CA 94598, USA
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/rpt_family="ALU"
complement (5422. .5707)
/note="85% similarity"
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complement(2544. .2843)
/note="85% similarity"
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6537. .21193
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complement (2896. 3191)
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/gene="CD22"
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                                           AUTHORS
TITLE
JOURNAL
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                     REFERENCE
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TVOILHSPAVEGGOVERLORGLANDLPTNYTWYHNGKEMOGERTEEKVHIPELIEWHAG
TYSCVARNILGTGORGPGAELDVOYPPKKYTTYLONPMPIREDTYTLECHYNSSNPS
VTRYEWKPHILGTGORGPGAELDVOYPPKKYTTYLONPMPIREDTYTLSCHYNSSNPS
VTRYEWKPHGAWEPPSLGVLIQUPFSSSHPKRYOPFWERVIGRLLGKESQLAMPDSISPEDA
RYRKIKPLSBIHSGNRYBLGVLYAPRELRVOFFWERVIGRLLGKESQLAMPDSISPEDA
SSYSCWYNNSIGGTASKAMTLEVLYAPRELRVSWSFGDQVWEGKSATLTCESDANPPV
SHYTWFORNNOSLEPHSQCARLEVLYAPRELRVSWSFGSYWSVGKRSRSPELTTYYSPE
TIGRRYAVGLGSCLAILILAIGGLKLQRRWKRTQSQCCLQENSSGGSFFVRNKKYRRA
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JOIN (6537). . 6570, 7043. . 7420, 10532. . 10837, 15337. . 15634,
15839. . 16102, 16198. . 16461, 19325. . 19421, 19547. . 19622,
20098. . 20216, 20647. . 20731, 21062. . 21193)
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CLLAPSCYGYP I QLQMLLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKIVT
CQLQDADGKEELSINDTVQLAVKHPPKKYTTVIQNPMPLREGDTVTLSCRYNSSNPSVTR
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KIKPLSE IHGGNSVSLQCDPSSSHPKEVQFWRKNGRLLGKESQLNFDS I SPEDAGSY
SCWVNNS I GQTASKAATLEVLYAPRRILRVSMSPGDQVMEGKSATLTCESDANPPVSHY
TWFDWNNQSLPYHSQKLRLEPVKVQHSGAXWCQGTNSVGKGRSPLSTLIVYXSPETIG
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EGPHSLGCYNPWMEDGISYTTLRFPEWNIPRTGDAESSEMQRPPPDCDDTVTYSALHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MHLLGPWLLLLVLEYLAPSDSSKWVPEHPETLYAWEGACVWIPC
TYRALDGDLESPILFHNPEYNKNTSKPDGTRLYESTKDGKVPSEQKRVQPLGDKNKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence deposited under GenBank
                                                                                                                                                                                                                                                                                                                                                                                                          /note="alternatively spliced; B-lymphocyte cell adhesion molecule; BL-CAM; human differentiation antigen; B-cell receptor CD22 precursor (alpha and beta)" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="B-cell receptor CD22-A isoform"

/protein id="AAB06449.1"

/db_xref="GI:1498646"
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Complement (13119. 13424)
/note="92" similarity"
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13457. 13745
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/rpt_family="ALU"
/rpt_family="ALU"
/note="87% similarity"
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/rpt_family="ALU"
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/gene="CD22"
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complement(8077. .8345)
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9293. .9591
/note="90% similarity"
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/note="89% similarity"
/rpt_family="ALU"
join[12252. .12472,1271
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9789. 10357
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11454. .11750
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16341
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                                                                                                                                                                                                                                                                                                                                                                                      /gene="CD22"
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PAT 12-JUN-2003
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Liaw, C.W., Behan, D.P. and Chalmers, D.T.
Non-endogenous, constitutively activated
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                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                           Patent: US 6553339-A 271 29-APR-2003;
Patent: US 6553339-A 271 29-APR-2003;
Location/Qualifiers
1. :003
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                903 bp Di
Sequence 271 from patent US 6555339.
AR308751
                                                                                                                                                                                                                                         GI:31700280
                                                                                                                                                                                                                                                                                                                             Unclassified.
                                                             26948 TAA 26950
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                    903
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Matches 903; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              CCTGCCCGCCTCAGTTTCTCCATCCTGCTCTTCTTCGTGCCCCTGGTCATCACCGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLC
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Patent: WO 02057783-A 3 25-JUL-2002;
Glaxo Group Limited (GB) ; Smithkline Beecham
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/mol type="unassigned DNA"
/db_xref="taxon:10090"
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Sequence 3 from Patent WO02057783.
AX675045
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/poduct="GPR40"
/product="GPR40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research Laboratories 1, Takeda Chemical Industries, Ltd.; Wadai 10, Tsukuba, Ibaraki 300-4293, Japan (E-mail:Hinuma_Shuji@takeda.co.jp, Tel:81-298-64-5035, Pars:81-298-64-5000)
Location/Qualifiers
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                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 903)
Shojif.F., Shoichi,O., Noguchi,Y., Itoh,Y., Kobayashi,M., Fujii,R.
and Hinuma,S.
Direct Submission
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Kobayashi, W., Pujii, K., Fukusumi, S., Tanaka, Y., Maruyama, M.,
Uejima, H., Satoh, R., Kizawa, H., Okubo, S., Ogi, K., Komatsu, H.,
Matsumura, F., Noguchi, Y., Fukatsu, K., Hinuma, S., Fujisawa, Y..
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Unpublished
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/db_xref="taxon:10036"
/cell_line="HIT-T15"
/cell_type="pancreatic beta
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                                    Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
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mouse) Chordata; Rodentia;

Eukaryota; Metazoa; Mammalia; Eutheria;

AB095745.1 GI:34392454

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Direct Submission
Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research
Laboratories 1, Takeda Chemical Industries, Ltd.; Wadai 10,
Tsukuba, Ibaraki 300-4293, Japan (E-mail:Hinuma_Shuji@takeda.co.jp,
Tel:81-298-64-5035, Fax:81-298-64-5000)
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Itoh,Y., Hosoya,M., Harada,M., Kawamata,Y., Tanaka,H.,
Kobayashi,M., Fujii,R., Fukusumi,S., Tanaka,Y., Maruyama,M.,
Uejima,H., Satoh,R., Kizawa,H., Okubo,S., Ogi,K., Komatsu,H.,
Matsumura,F., Noguchi,Y., Fukatsu,K., Hinuma,S., Fujisawa,Y.
Fujino,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.9%; Score 604.4; DB 10; Best Local Similarity 79.4%; Pred. No. 1.3e-85; Matches 716; Conservative 0; Mismatches 186;
                                                                                                                                                                                                                        Expression of GPR40 in pancreatic cells Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1. .903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="GPR40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .903
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ROD 02-SEP-2003

linear

bp mRNA complete cds.

AB095745 903 Mus musculus mRNA for GPR40, AB095745

RESULT 10
AB095745
LOCUS
DEFINITION
ACCESSION

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/procedi_id="AAN03478.1"

/db_xref="GI:22597182"

/db_xref="GI:22597182"

/db_xref="GI:22597182"

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KILRAAWVAGGALLFLLCLGCPYNASFINPDLGGSWRKLGLITGAWSVVLNPLVT

GYLGTGPGRGTICVTRTQRGTIQK"
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Larity 79.3%; Pred. No. 1.9e-85;
Conservative 0; Mismatches 187;
   'mol_type="genomic DNA"
(strain="BALB/c"
                                                                'db_xref="taxon:10090"
                                                                                  <535. >1437
/gene="Gpr40"
<535. >1437
/gene="Gpr40"
/product="GPR40"
                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="GPR40"
                                                                                                                                                                                                                                         35. .1437
/gene="Gpr40"
                                                                                                                                                                                                                                                                                                   note="GPCR"
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nes 715; Conserv
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Andrews, J. L., Briscoe, C.P., Ignar, D.M., Muir, A.I., Sauls, H.R. Jr. and Tadayyon, M. Method of Screening for GPR40 Ligands
Method of Screening for GPR40 Ligands
Patent: PCT WO/02/057783-B 25-UUL-2002;
Glaxo Group Limited; Glaxo Wellcome House, Berkely Avenue;
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Briscoe, C.P., Tadayyon, M., Andrews, J.L., Benson, W.G.,
Chambers, J.K., Eilert, M.M., Ellis, C., Elshourbagy, N.A., Goetz, A.,
Minnick, D.T., Murdock, P.R., Sauls, H.R. Jr., Shabon, U.,
Spinage, L.D., Strum, J.C., Szekeres, P.G., Tan, K.B., Way, J.M.,
Ignar, D.M., Wilson, S. and Muir, A.I.

The orphan G protein-coupled receptor GPR40 is activated by mediand long-chain fatty acids
J. Biol. Chem. 278 (13), 11303-11311 (2003)
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Submitted (01-AUG-2002) Metabolic Diseases, GlaxoSmithKline,
Moore Drive, Durham, NC 27709, USA
Location/Qualifiers
1. 1819
/organism="Mus musculus"
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Mus musculus GPR40 (Gpr40) gene, complete cds.
AF539809
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Ellis, C. and Elshourbagy, N.
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/db_xref="texon:10090"
/clone="R23-2229"
/clone_lib="RPCI mouse BAC library 23"
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Consensus quality: 180765 bases at least Q40
Consensus quality: 200208 bases at least Q30
Consensus quality: 200208 bases at least Q30
Estimated insert size: 186000; agarose-fp estimation
Estimated insert size: 207873; sum-of-contigs estimation
Quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation
(Quality coverage: 7.41 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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1195 AGGCAGCTTGGGTGGCCGGAGGCGCTCTCCTCACACTCCTGCTCTGCCTGGGGCCCTAT 1254
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Submitted (09-DEC-2000) Production Sequencing Pacility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mus musculus clone RP23-22G9, WORKING DRAFT SEQUENCE, 21 unordered
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Sciurognathi; Muridae; Musinae; Mus.
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1953: gap of unknown length
2957: contig of 1004 bp in length
3957: gap of unknown length
4549: contig of 1492 bp in length
4649: gap of unknown length
6366: contig of 1717 bp in length
6466: gap of unknown length
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Center clone name: RPCI-23_22G9
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Center: Joint Genome Institute
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Mammalia, Butheria, Rodentia,
1 (bases 1 to 209873)
DOB Joint Genome Institute.
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AC087143.1 GI:11610869
HTG; HTGS PHASB1; HTGS_DRAFT.
Mus musculus (house mouse)
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DOE Joint Genome Institute.
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Mus musculus clone RP23-123D23, WORKING DRAFT SEQUENCE, 34
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Direct Submission

Submitted (102-SPR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center
Center: Joint Genome Institute
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DOB Joint Genome Institute.
Sequencing of Mouse
                                                                                            106687 AACATACCCGTGAATGGCTCCCCGGTCTGGCAGAGCCTGGGATCCCGACTCTGCCCGC
GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGCTGGACCACAGCAACACCTCCCTGGGCATC
                                                                                                                                            CCGGCCCGCTTCAGCCTCTCTCCTGCTCTTTTTTCTGCCCTTGGCCATCACAGCCTTC
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                                                                     <u>AACACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTTGTGCCGGC</u>
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Consensus quality: 141366 bases at least Q30
Consensus quality: 14402 bases at least Q20
Estimated insert size: 221980; agarose-fp estimation
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Mus musculus (house mouse)
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DOE Joint Genome Institute.
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Quality coverage: 9.04 in Q20 bases; agarose-fp estimation Quality coverage: 13.25 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
Estimated insert size: 151373; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                      gap of unknown length
contrig of 1439 bp in length
contrig of 1439 bp in length
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gap of unknown length
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contrig of 1189 bp in length
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of 1396
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gap of
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11148:
2687:
3845:
3945:
5134:
6339:
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23825:
26327:
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40399:
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20654:
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contig of 6900 bp in length
gap of unknown length
contig of 12384 bp in length
gap of unknown length
contig of 8411 bp in length
gap of unknown length

contig of 6860 bp in length gap of unknown length contig of 5611 bp in length gap of unknown length unknown length of 6900 bp in length

96071: 102971:

unknown length of 6860 bp in length

83400:

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/procein_id="BAC82554.1"
/db_xref="G1:34392453"
/translation="MDLPPQLSFALYVSAFALGFPLNLLAIRGAVSHAKLRLTPSLVY
TLHIACSDLLIAITPERAVEALASGVWPLPPEPPCPVFPLAHFAPLYAGGGFLAALSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRYLGAAFPFGYQAIRRPCYSWGVCVAIWALVLCHLGLALGLEAPRGWVDNTTSSLGI
IDYWGSPYCLLEAWDPDSARPRALSFSILLFPLLDIYITAFCYVGCLRALVHSGLSHKR
KLRAMVAGGALLTLLCLGPYNASFINPDLEGSWRKLGLITGAMSVVLNPLVT
GYLGTGPGGGTICTFLTRPRGTIQK"
                                                                                                                                                                                 02-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (08-NOV-2002) Shuji Hinuma, Discovery Research
Laboratories 1, Takeda Chemical Industries, Ltd.; Wadai 10,
Tsukuba, Ibaraki 300-4293, Japan (E-mail:Hinuma_Shuji@takeda.co.jp,
Tel:81-298-64-5035, Fax:81-298-64-5000)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 903)
Shoji,F., Shoichi,O., Noguchi,Y., Itoh,Y., Kobayashi,M., Pujii,R.
and Hinuma,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                    114992 ACAGGTCCTGGACGGGAACAATATGTGTGACGAGGACTCAAAGAGGAACATTC 115045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGCCCACGCCCGGCTCCGTCTCACCCCT
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Kobayashi,M., Pujii,R., Fukusumi,S., Tanaka,Y., Maruyama,M.,
Uejima,H., Satoh,R., Kizawa,H., Okubo,S., Ogi,K., Komatsu,H.,
Matsumura,F., Noguchi,Y., Fukatsu,K., Hinuma,S., Fujisawa,Y.
                           894
                           841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAAGGCAAGGGGGCAAGTCC
                                                                                                                                                                                 ROD
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                                                                                                                                                                              mRNA linear complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 590; DB 10; Length 9
Pred. No. 2.3e-83;
0; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression of GPR40 in pancreatic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                                                          Rattus norvegicus mRNA for GPR40, AB0055744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /moi_type="mRNA"
/db_xref="taxon:10116"
1. .903
                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="GPR40"
                                                                                                                                                                                                                                            AB095744.1 GI:34392452
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Best Local Similarity 78.4%;
Matches 707; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, .903
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                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                   RESULT 14
AB095744
LOCUS
DEFINITION
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JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114932 GGACTCATCACAGGGCCCTGGAGTGTGGTACTCAACCCACTGGTCACTGGCTACTTGGGA 114991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGCTGGACCACAGCAACACCTCCCTGGGCATC
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                             66.2%; Score 598; DB 2; Length 154673; 79.3%; Pred. No. 4.4e-85; ive 0; Mismatches 185; Indels 0;
132993: contig of 8927 bp in length
133093: gap of unknown length
142772: contig of 9679 bp in length
142872: gap of unknown length
154673: contig of 11801 bp in length.
                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-123D23"
/clone_lib="RPCI mouse BAC library 23"
                                                                                                              Location/Qualifiers
1. .154673
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.3
Matches 709; Conservative
                    132994
133094
142773
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                                                                    Diseases, GlaxoSmithKline,
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Best Local Similarity 78.4%; Pred. No. 2.3e-83;
Matches 707; Conservative 0; Mismatches 195; Indels
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Unpublished
3 (bases 1 to 907)
Blis, C.E. and Elshourbagy, N.
Direct Submission
Submitted (01-AUG-2002) Metabolic Dis
Moore Drive, Durham, NC 27709, USA
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Briscoe, C.P., Tadaryon, M., Andrews, J.L., Benson, W.G.,
Chambers, J.K., Eilert, M.M., Ellis, C., Elshourbagy, N.A., Goetz, A.S.,
Minnick, D.T., Murdock, P.R., Sauls, H.R., Jr., Shabon, U.,
Spinage, L.D., Strum, J.C., Szekeres, P.G., Tan, K.B., Way, J.M.,
Ignar, D.M., Wilson, S. and Muir, A.I.
The orphan G protein-coupled receptor GPR40 is activated by medium
and long-chain fatty acids
J. Biol. Chem. 278 (13), 11303-11311 (2003)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
 AGGGCAGCTTGGGTGGTGGAGGAGCACTTCTCTCACACTCCTGCTCTGCCTGGGGGCCCTAT
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AF539810.1 GI:22597102
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Ellis, C.E. and Elshourbagy, N.
Rat GPR40 cDNA
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841 AGGGGTCCTGGCCTGAAGACAGTGTGCGGCAAGAACGCAAGGGGGCAAGTCCCAGAAG 900
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

April 30, 2004, 07:46:59; Search time 452 Seconds (without alignments) 8486.997 Million cell updates/sec

US-10-202-687-1 903 Title: Perfect score:

1 atggacctgccccgcagct......ggggcaagtcccagaagtaa 903 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched:

6747726 Fotal number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\*geneseqn2003bs:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2003cs:\* N\_Geneseq\_29Jan04:\* geneseqn1980s:\* geneseqn1990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

SUMMARIES

## Re

Description	Aaa30759 Human G p	Abk90236 Human cDN	Abz42843 Human G p	Adc22768 Human G p	Adb61405 DNA encod	Aaa30776 DNA encod	Adc22790 Human G p	Adb61417 DNA encod	Adb61429 DNA encod	Abk90237 Mouse cDN	Adb61401 DNA encod	Adb61403 DNA encod	Aav53631 Human 7-t	Aaa30762 Human G p	Aah26460 Human G-p	Aah26459 Human G-p	Abz42561 Human G p	Adc22772 Human G p	Aaa30777 DNA encod	Adc22792 Human G p	Aax90981 Human pro	Aaa35309 Human ade	Aaf21431 Human low
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DB	6	9	7	σ	σ	m	σ	σ	σ	9	σ	σ	~	М	4	4	~	σ	m	σ	N	m	٣
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Query Match	100.0	100.0	100.0	100.0	7.66	99.5	99.5	93.1	67.8	6.99	66.7	65.1	13.7	13.5	13.5	13.5	13.5	13.5	13.1	13.1	9.4	9.4	4.
Score	903	903	903	903	900	898.2	898.2	840.8	612	604.4	602.4	588	123.4	121.8	121.8	121.8	121.8	121.8	118.6	118.6	84.6	84.6	84.6
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## ALIGNMENTS

AAA30759 standard; cDNA; 903 BP. 21-AUG-2000 (first entry) AAA30759; RESULT 1 AAA30759 

Human G protein-coupled receptor GPR40 cDNA.

G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; ss.

Homo sapiens.

WO200022129-A1.

20-APR-2000.

99WO-US023938. 12-OCT-1999;

98US-00170496 13-OCT-1998;

(AREN-) ARENA PHARM INC

Liaw Chalmers DT, Behan DP,

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WPI; 2000-329165/28. P-PSDB; AAY90679.

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents.

Example 1; Page 307; 341pp; English.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90681-Y90681), and to DNA encoding them (AAA30709-A30703 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (CIG) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X- (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or

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LE Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be condopenous, non-endopenous, or a mixture of endogenous and non-endopenous contained and partial agonists are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical companies. The mutant proteins are also useful in research settings for clucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and clisometra seconds with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence compounds without the need for endogenous ligands. The present sequence compounds without have nown wild-type GPCR used in an exemplification of the invention. This was cloned and subjected to sitedirected mutagenesis (SDM) to generate DNA encoding the corresponding the curresponding compand to the invention.
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Sequence 903 BP; 108 A; 327 C; 283 G; 185 T; 0 U; 0 Other;

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 Length 903;
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Score 903; DB 3;
Pred. No. 2e-167;
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100.0%;
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Human; ss; gene; GPR40; G protein-coupled receptor; type 2 diabetes; obesity; antidiabetic; neuroprotective; anorectic; cerobroprotective; Gq; G protein; reporter gene; glucose intolerance; insulin intolerance; neurodegenerative disease; Alzheimer's disease; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GRR40 ligand to a GPR40 receptor. Also included are (1) a method of screening a compound for GPR40 antagonist activity, comprising; (a) measuring any detectable signal produced by a reporter gene (comprising a reporter gene under the control of G protein Gq responsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist; or (c) detecting whether the compound decreases glucose-stimulated insulin release from mammalian pancreatic beta cells in the presence of a GPR40 agonist; (2) a method of screening a compound for GPR40 agonist; (2) a method of screening any
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721 AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGCTCCTGGCGGAAGCTG 780
                                                                                                                       841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAACGCAAGGGGGGCAAGTCCCAGAAG
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GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2 diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence is the human cDNA for GPR40
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or aridity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody seaned of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, or autoimmune diseases, growth-related diseases, cell regeneration-related diseases, cell are therosclerosis, bacterial, fungal, prococoan or viral infections, osteoprorosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, graft versus host antiet, antiet, depression, schizophrenia, debenetia, memory classes, epilepsy, asthma, tuberculosis, obseivy, nausea, hypertension, or anxiety, or candiomyopathy, rausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; grotein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; call regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nauses; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                      Human G protein-coupled receptor GPR40 nucleotide SEQ ID NO:474.
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any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42669 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that transmembrane-6 (TM6) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive cartivity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonises or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing
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                                                                                                                                                                                                                                                                                                          Human; gene; ss; G protein-coupled receptor; GPCR;
transmembrane-6 region; TM6; intracellular-3 region; IC3.
                                                                                                                                                                                                                                 Human G protein-coupled receptor cDNA #36.
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98US-00060188.
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ADC22768 standard; cDNA; 903
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Matches 903; Conservative
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          CGCTCAACGTCCTGGCCATCCGAGGGGGAGGCCCACGCCCGGCTCCGTCTCACCCCT
                            AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCC
                                          AGCCTGGTCTACGCCCTGAACCTGCTGCTCCGACCTGCTGACAGTCTCTGCCCC
                                                                       GTCTTCGCGGTGGCCCACTTCTTCCCACTCTATGCCGGCGGGGGCTTCCTGGCCGCCCTG
                                                                                                                  AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, entiarteriosclerotic, antiarthritic, osteopathic, thrombolyvic, nootropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and clarker compositions can be used in the treatment, prevention and diaphetic retinopathy, hyperlipaemia, skin diseases, compinately, diabetic retinopathy, hyperlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin allergy, fat metabolism disorders and cancer. This polymulectide sequence represents the DNA encoding a human GPR40 protein
                       osteopāthic; thrombolytīc; nootropic; anorectic; hypotensive; cytostatic; diabetes; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; diabetic retinopathy; hyporlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hyportrension; indigestion; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; human; gene; ds.
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antilipaemic; dermatological; antiarteriosclerotic; antiarthritic;
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Y, Ogi K, Harada M, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Human GPR40 protein"
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fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological;

DNA encoding human GPR40 protein.

(first entry)

04-DEC-2003

ADB61405

ADB61405 standard; DNA; 900

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Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical

agents.

Liaw CW;

Chalmers DT,

Behan DP,

WPI; 2000-329165/28 P-PSDB; AAY90684

(AREN-) ARENA PHARM INC

98US-00170496.

12-OCT-1999; 20-APR-2000.

> protein-coupled receptor; GPCR; constitutively active; ntracellular loop 3; transmembrane domain 6; drug screening; agonist; DNA encoding human mutant G protein-coupled receptor GPR40 (A223K) AAA30776 standard; DNA; 903 (first entry) antagonist; mutant; ss. intracellular 21-AUG-2000 Homo sapiens Synthetic. AAA30776;

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90693-AAY90693-AAY90693-AAY90693-AAY90693-AAY90693-AAY90693-AAY9073 and AAY90693-Y90687), and to DNA encoding them (AAA30775-AA9079). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid N-terminal of an endogenous proline in TM6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous creatiques. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical creatiques the roles of the receptors in normal and diseases and discating the roles of the receptors in normal and diseases and discates associated with that receptors. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30779-CAAA30779 represent DNAS encoding the mutant human
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99.7%; Pred. No. 1.7e-166;
iive 0; Mismatches 3;
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AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG

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WO200022129-A1

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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TM6) region and an an intracellular-3 (IC3) region, by substituting a specific amino acid in the TM6 region with a different amino acid, and testing for constitutive cativity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a ligand for the receptor. This is particularly useful in allowing conservant or screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents conding a human GPCR.
                           Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.5%; Score 898.2; DB 9;
Best Local Similarity 99.7%; Pred. No. 1.7e-166;
Matches 900; Conservative 0; Mismatches 3;
                                                                                                  Example 2; SEQ ID NO 271; 221pp; English
                                                                        constitutive activity
P-PSDB; ADC22791.
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transmembrane-6 region; TM6; intracellular-3 region; IC3.
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98US-00060188.
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                    acid; eicosanoid-binding G-protein coupled receptor; GPR40;
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Y, Ogi K, Harada M, Fukusumi S;
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/note= "No stop codon"
/product= "Monkey GPR40 protein"
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                                                                                                                                                                                                                                                                                                                                             DNA encoding monkey GPR40 protein.
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                                                                                                                                                                                                                                                                                    ADB61417 standard; DNA; 900 BP
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12-JUL-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and eicosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antidipaemic, dermatological, antidipaemic, correctic, hypotensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyporlypaemia, skin disease, chiabetic retinopathy, hyporlypaemia, skin disease, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigetion, menory loss, obesity, hypoglycaemia, edema, insulin resistance, insulin allergy, fat metabolism disorders and cancer. This protein of the invention.
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Pred. No. 2.9e-155;
0; Mismatches 37;
                                                                                     Claim 12; Page 241-242; 257pp; Japanese.
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95.9%;
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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences tully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, nabbolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarteriosclerotic, antiarthritic, osteopathic, thrombolytic, noctropic, anorectic, hypotennive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyperlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, nebrotathy, and sequence represents the DNA encoding a hamster GPR40 protein of the invention.
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Fukusumi S;
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Kawamata Y, Ogi K, Harada M,
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/product= "Hamster GPR40 protein"
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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Kizawa H,
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The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor. Also included are (1) a method of screening a compound for GPR40 antagonist activity, comprising; (a) measuring any detectable signal produced by a reporter gene (comprising a reporter gene under the control of G protein GG responsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist; or (c) detecting whether the compound decreases glucose-stimulated insulin release from mammalian pancreatic beta cells in the presence of a GPR40 agonist; compared to glucose-stimulated insulin release to the presence of the GPR40 agonist; (2) a method of screening any compound for GPR40 agonist; (a) method of screening any
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                                                                                                                         GGGCTCATCACAGGGTCCTGGAGTGTGGTACTCAACCCGCTGGTCACCGGTTACTTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits tbinding of a fatty acid GPR40 ligand to a GPR40 receptor.
AGGGCAGCCTGGGCGGCCGGAGGGGCCTTTCTCACACTCCTGCTTGGGGCCCCTAC
                                                      AGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAAAGAGGGGGCAAGTCCCAGAAG
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                   GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2 diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence is mouse cDNA for GPR40
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                                                                                                                                                                                                 fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological, antiarteritor; antiartrhitic; osteopathic; thrombolytic; nootropic; anorectic; hypotenaive; cytostatic; diabetic thrombolytic; nootropic; anorectic; hypotenaive; cytostatic; diabetic retinopathy; hyperlipaemia; skin disease; arthitis; bone disease; arteriosclerosis; thrombosis; hyportension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; mouse; murine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the nephrotropic, ophthalmological, antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarthritic, osteopathic, thrombolyric, anostropic, antiarthritic, osteopathic, thrombolyric, and eicosanoid-binding G-protein coupled receptor protein, GPR40, and further compositions can be used in the treatment, prevention and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic
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Kawamata Y, Ogi K, Harada M, Fukusumi S;
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/product= "Mouse GPR40 protein"
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                                                                                                                                                                              encoding mouse GPR40 protein
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12-JUL-2002; 2002JP-00261163.
12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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                                                                                                                                                                                              Sequence 900 BP; 137 A; 300 C; 244 G; 219 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               Score 602.4; DB 9;
Pred. No. 1.1e-108;
0; Mismatches 186;
                                                                                                                                                                                                                                                 tch 66.7%;
al Similarity 79.3%;
714; Conservative
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Best Local S:
Matches 714,
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamster (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarteriosclerotic, antialipaemic, dermatological, antiarteriosclerotic, antiarthritic, osteopathic, thrombolytic, ancertic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and factosanoid-binding G-protein coupled receptor protein, GPR40, and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyporlipaemia, skin diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin createner, mentanoe, innulin allergy, fat metabolism disorders and cancer. This polynucleotide sequence represents the DNA encoding a rat GPR40 protein of the invention.
                                                                                                                                                                                      fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological; antiarteritosic; antiarthritic; osteopathic; thrombolytic; nocropic; anorectic; hypotensive; cytostatic; diabetic; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; bone disease; arthritis; bone disease; arteriosclerosis; thrombosis; hypotension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; rat; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fatty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.
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Kawamata Y, Ogi K, Harada M, Fukusumi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No stop codon"
/product= "Rat GPR40 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .900
                                    ADB61403 standard; DNA; 900 BP
                                                                                                                                                      encoding rat GPR40 protein
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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Kizawa H,
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                                                                                  Length 900;
                             Sequence 900 BP; 142 A; 287 C; 244 G; 227 T; 0 U; 0 Other;
                                                                            Score 588; DB 9; Length 90
Pred. No. 7.3e-106;
0; Mismatches 195; Indels
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78.3%;
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Best Local Similarity
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AAV53631

513 257 573

137 453 377

437 753 497

317 633

(first entry)

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Sequence 1841 BP; 334 A; 538 C; 593 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                     HNFDY20 activity or levels are also provided
               Human 7-transmembrane receptor HNFDY20 cDNA,
                                                                                                                                                                                                    Claim 3; Page 2-4; 24pp; English,
                                                                                                                                        SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.3
Matches 383; Conservative
                                                                                                                                                  Bergsma DJ, Sathe GM,
                                                                                                                                                            WPI; 1998-482962/42
                                                                                                                                                                  P-PSDB; AAW59924.
                                                                  Homo sapiens
                                                                                                                    16-FEB-1998;
                                                                                                                              19-MAR-1997;
     07-DEC-1998
                                                                                               EP866126-A1
                                                                                                          23-SEP-1998
                                                                                                                                                                                                                     human
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13.7%; 52.3%;

18

ઠ 셤

Mao JY;

Fuetterer WS,

98EP-00301122 97US-00820521

Location/Qualifiers 125. .1330 /\*tag= a

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678 CGGCGGGGCCCTCCTCACGCTGCTCTGCGTAGGACCCTACAACGCCTCCAACGTGGC 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   634 dadretredecenececererregracandancecedecendecendecadecenderecentered 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754 CTCAGGGG------ACATCTCCCACAGGCCAGGCAATGGGACTG 795
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intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                     198 GCTAGCCTCCGGGGCCTGGCCTCTGCGGCCTCGCTGTGCCCCGTCTTCGCGGTGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 CATCCGAGGCGCGCGCCCCACGCCCCGGCTCCGTCTCACCCCTAGGCCTGGTCTACGCCCT
                                                    394 ceregredeterregredechagergebedecececegegegegegegegeneere
                                                                                                                  138 GAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGTGGAGGC
                                                                                                                                                                          454 CAACCTGACCGCCTCGGACCTGCTCCTGCTGTTCCTGCCTTTCCGCATGGTGGAGGC
                                                                                                                                                                                                                                                                                                514 AGCCAATGGCATGCACTGGCCCTTCATCCTCTGCCCACTCTCTGGATTCATCTT
                                                                                                                                                                                                                                                                                                                                                           CTTCTTCCCACTCTATGCCGGCGGGGCTTCCTGGCCGCCCTGAGTGCAGGCCGCTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCGTGCTATTCCTGGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 TCCAGGAGGCTGGCTGGACCACAGCAACACTCCCTGGGCATCAACACACGGTCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558 CTCTCTCCTGCTCTTTTTTCTGCCCTTGGCCATCACAGCCTTCTGCTACGTGGGCTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               testis and human liver using expressed sequence tag analysis. The invention relates to HNFDYZO polypeptides and recombinant materials and methods for their production. It also provides methods for using such polypeptides and HNFDYZO polypeptides of infections such polypeptides and HNFDYZO polypucleds for treatment of infections such polypeptides and HNFDYZO polypucleds for treatment of infections such infections, fungal, protozoan and particularly HIV-1 or HIV-2 infections, and conditions including pain, cancers, anorexia, asthma, Parkinson's disease, acute heart failure, hypotension, hypotension, curinary retention, osteoporosis, angina pectoris, myocardial infarction, utinary retention, osteoporosis, angina pectoris, myocardial infarction, curinary retention, demontia, severe mental retardation and dyskinesias, such as Huntingdon's disease or Gilles de la Tourette's syndrome. Gene therapy using RNA encoding HNRDYZO can be used to treat conditions caused by under-expression of the protein. The invention also relates to methods of identifying agonists and antagonists and for using such compounds to treat conditions associated with inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s isolated polynucleotide codes for HNFDY20 (see AAW59924), a novel an 7-transmembrane G-protein coupled receptor. HNFDY20 polynucleotides be obtained from cDNA libraries derived from mRNA in cells of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GTTCGTCTTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAACCTGCTGGC
                                                                                                                                        HNFDY20; G-protein coupled receptor; human; infection; HIV; pain; cancer; ansthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; mental retardation; dyskinesia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; ss. Gilles de la Tourette's syndrome; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treating eg cancer, osteoporosis and Parkinson's disease and infections caused by HIV-1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTGGGCTTCCCGCTCAACGTCCTGGC
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Pred. No. 4.7e-15;
0; Mismatches 326; Indels 24;
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696

617

909 677

Liaw CW;

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY96643-AAY9069-190687), and to DNA encoding them (AAA30709-A330743) and AAA30775-A30779). The mutant proteins of the invention contain a matation in a portion of the protein comprising intracellular loop 3 (CC) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous creatiques. The constitutively active GPCRs are useful for identifying antagonists and partial agonists for use as pharmaceutical captured are also useful in research settings for a particular GPCR are useful for treating diseases and disorders associated with that receptors in normal and diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence compounds without the need for endogenous ligands. The present sequence crepresents cDNA encoding a human wild-type GPCR used in an expensive for invention. This was cloned and subjected to site-directed mutagenesis (SDM) to generate DNA encoding the corresponding the corresponding mutant of the invention Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical Example 1; Page 309-310; 341pp; English. (AREN-) ARENA PHARM INC Chalmers DT, WPI; 2000-329165/28. P-PSDB; AAY90680. Behan DP, agents. 

Sequence 1041 BP; 170 A; 324 C; 315 G; 232 T; 0 U; 0 Other;

344 137 164 197 257 317 GGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCGTGCTATTCCTGGGGGGT 377 404 Grececeaccarcreseccercercreserecresereresererreserreserreserreseres 437 GAGTGTGGCCTGCTGGCTGTTGGCCTCTGCTCACTGCAGCGTGGTCTACGTCATAGAATT 464 GTTCGTCTTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAACCTGCTGGC 104 165 CAACCTGACCGCCTCGGACCTGCTCCTGCTGTTCCTGCCTTTCCGCATGGTGGAGGC 224 225 AGCCAATGGCATGCACTGGCCCTTCATCTTCTGCCCACTCTCTTGGATTCATCTT 284 77 105 CCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCCCGGTGGCCGTGGACGTGCTCCTGCT circaccaccarciarcrcaccaccrciriccicaccacigidadearraaaccirirci CATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT 138 GAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGTGGAGGC GCTAGCCTCCGGGGCCTGGCCCTCTGCCGGCCTGTGCCCCCGTCTTCGCCGGTGGCCCCA CTTCTTCCCACTCTATGCCGGCGGGCTTCCTGGCCGCCCTGAGTGCAGGCCGCTACCT GCTCTCCTTCGGCCTTATGTGGCCGCCTTTGCGCTTGGGCTTCCCGCTCAACGTCCTGGC Gaps 24; Score 121.8; DB 3; Length 1041; Pred. No. 9.4e-15; 0; Mismatches 327; Indels 24; 13.5%; 52.1%; Best Local Similarity 52.1 Matches 382; Conservative Query Match 18 45 78 198 285 318 345 258 ò g ઠે 셤 ઠે a 셤 ઠે 셤 ò ద δ ઠ

The present sequence is that of cDNA encoding human G-protein coupled receptor 42 (GPR 42, see AAB82759). The invention is based on the finding that expression of GPR 42 and GPR 41 (see AAB82758) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting lipolysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 activity, involving: (1) contacting a test agent with GPR 41 or GPR 42 or a variant capable of

740 557 563 617 620 680 TCCAGGAGGCTGGCTGGACCACAGCAACACCCTCCCTGGGCATCAACACACGGTCAACGG 497 ---ACATCTCCCACAGCCAGGCACCAATGGGACCTG 506 CCGGGCACTGGCCCGCCTCCGGCCTGACGCACAGGCGGAAGCTGCGGGCCGCCTGGGTGGC 617 678 GGGGGGGCCCTCCTCACGCTGCTCTGCGTAGGACCCTACAACGCCTCCAACGTGGC 737 GPR 42; G-protein coupled receptor 42; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; sandrome X; antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; gene therapy; ss. stoke. 681 GGCGGCCACGCTGCTCAACTTCCTTGTCTGTTTGGGCCCTACAACGTGTCCCATGTCGT 507 CTACCTGGAGTTCCGGAAGGACCAG--CTAGCCATCCTCCTGCCCGTGCGGCTGGAG-AT CICICICCIGCICITITITICIGCCCTIGGCCATCACAGCCTTCTGCTACGTGGCTGCCT 564 gechergencenchringregicedechandarchichengenacherhachen-Ageedeen genérogancenciade a gada de a consecuencia de consecue CTCTCCGGTCTGCCTGGAGGCCTGGGACCCGGCCTCTGCCGGCCCGGCCCGGCTTCAGCCT Identification of an agent for the modulation of G-protein coupled receptor useful for the treatment of disease i.e. dyslipidemia or a Human G-protein coupled receptor GPR 42 cDNA. Claim 16; Page 46-47; 53pp; English. AAH26460 standard; cDNA; 1041 BP 18-FEB-2000; 2000GB-00003900. 22-MAR-2000; 2000GB-00007015. 19-FEB-2001; 2001WO-GB000684. 738 CAGCTTCCTGTAC 750 741 GGGCTATATCTGC 753 (first entry) (GLAX ) GLAXO GROUP LTD 2001-536581/59 Brown AJ; 465 CTCAGGGG-P-PSDB; AAB82759 WO200161359-A2 Homo sapiens, 29-OCT-2001 23-AUG-2001. 618 558 AAH26460; 498 **Wise A**, AAH26460 셤 ò 셤 ò 엄 ð 엄 8 ద ઠે 셤 

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in the presence of a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41 or GPR 42 or uninhibitor of lipolysis, or a polymucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dyslipideamia, coronary heart disease, atherosclearosis, thrombossis or obesity, angina, chronic renal failure, peripheral vascular disease, stroke, type II diabetes or metabolic syndrome (syndrome X) (all claimed)
                                                                                                                                                                                                                                                                                                         45 GTTCGTCTTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAACCTGCTGGC 104
                                                                                                                                                                                                                                                                                                                                             CATCCGAGGCGCGGACGCCCACGCCCGGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                    GAACCTGGGCTGCTGCTGCTGCTGACAGTCTCTGCCCCTGAAGGCGGTGGAGGC 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681 GGGGCCACGCTGCTCCTTGTCTGCTTTGGGCCCTACAACGTGTCCCATGTCGT 740
 coupling to a G-protein; and (2) monitoring for GPR 41 or GPR 42 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 CAACCTGACCGCCTCGGACCTGCTCCTGCTGTTCCTGCCTTTCCGCATGGTGGTGGGC 224
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                                                                                                                                                                                             Score 121.8; DB 4; Length 1041;
Pred. No. 9.4e-15;
0; Mismatches 327; Indels 24;
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52.1%;
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C C C C C C C C C C C C C C C C C C C	c c c c c c c c c c c c c c c c c c c	0 0 0 0 0 0 0 0 0 0 0 0 0	000 0 0 0 00000000000000000000000000	RESULT 1 AY411510 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS
GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: April 30, 2004, 14:33:11; Search time 2948 Seconds (without alignments)	Title:  Perfect score: 903 Sequence: 1 atgacctgccccgcagctggggcaagtcccagaagtaa 903 Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 27513289 seqs, 14931090276 residues	Total number of hits satisfying chosen parameters: 55026578 Minimum DB seq length: 0 Maximum DB seq length: 2000000000  Post-processing: Minimum Match 0% Listing first 45 summaries	Database: EST:*  1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estvy:* 6: em_estpy:* 7: em_estpy:* 10: gb_est1:* 11: gb_htc:* 13: gb_est2:* 14: gb_est3:* 14: gb_est5:*	15: em_estfun:*  16: em_estom:*  17: em_gsstom:*  18: em_gss_inv:*  20: em_gss_inv:*  21: em_gss_vin:*  22: em_gss_vin:*  23: em_gss_mam:*  24: em_gss_mam:*  25: em_gss_phg:*  26: em_gss_phg:*  27: em_gss_vin:*  29: gb_gss2:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  No. Score Match Length DB ID  1 901.4 99.8 903 29 AY411510  2 823.6 91.2 834 29 AY411511  3 622.8 66.8 903 29 AY411512  AY411512 Mus muscu 4 376.8 41.7 443 10 AWS83167 AWS83167 ialffll.y

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6.34 DNA linear GSS 16-DEC-2003
Pan troglodytes GPR40 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY411511
                                                   841 AGGGGTCCTGGAGACAGTGTGTGCGCGCAAGAACGAAGGGGGGCAAGTCCCAGAAG 900
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                             841 AGGGGTCCTGGCCTGAAGACAGTGTGTGCGGCAAGAACGCAAGGGGGGCAAGTCCCAGAAG
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    .834
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

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/gene="GPR40"
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                            /gene="GPR40"
/locus_tag="HCM4248"
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Best Local Similarity 99.9%;
Matches 902; Conservative
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Mus musculus GPR40 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Rerifara, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. P. Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                     GTCAACGCTCTCCCGGTCTGCCTGGGACCCCGGCCTCTGCCGGCCCGC
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                                                                                                                                                                                                                                                                                                                                                                       DB 29; Length 903;
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                                                                                                                                                                                                                                                                                                                                                  66.8%; Score 602.8;
llarity 79.3%; Pred. No. 6.3e
Conservative 0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1. .>903
/gene="GPR40"
/locus_tag="HCM4248"
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CE730455 522 bp DNA linear GSS 30-SEP-2003
tigr-gss-dog-17000315416692 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                         TCTGCGTAGGACCCTACAACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAG 763
                                                                                                                                                      241 GCTCCTGGCGGAAGCTGGGGCTCATCACGGGTGCCTGGAGTGTGGTGCTTAATCCGCTGG 300
                                                                                                                                                                                                                                                         61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCCACGCCCCGGCTCCGTCTCACCCCT 120
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1 (bases 1 to 522)
1 (kixness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                   181 TCTGCGTAGGACCCTACAACGCCTCCAACGTGGCCAGCTTCCTGTACCCCCAATCTAAGAG
                                                                                                                         GCTCCTGGCGGAAGCTGGGGCTCATCACGGGTGCCTGGAGTGTGTGCTCTTAATCCGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003) 22875432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%; Score 306; DB 29;
86.0%; Pred. No. 7.6e-44;
iive 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence. CE730455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE730455.1 GI:37070575
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Canis familiaris
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Best Local Similarity 86.0
Matches 339; Conservative
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SOURCE
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CE730455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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/organism="Homo sapiens"

/organism="Homo sapiens"

/organism="mRNA"

/db xref="taxon:566"

/clone="IMAGE:5638029"

/tissue_type="rallets of Langerhans"

/dev stage="Adult"

/lab_host="DH10B"

/clone lib="Human Pancreatic Islets"

/clone lib="Human Pancreasi Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Primary library.
                                                                                                                         EST 13-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tail: 617-495-1812

Fax: 617-495-8557

Email: dmellon@blohp.harvard.edu

Libraries were constructed by Dr. Douglas Melton

DNA sequencing by: Washington University Genome Sequencing Center

For information on obtaining a clone please contact: Juliana Brown

Chrown@fas.harvard.edu)

This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 443)

Metlon, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and
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121 CGCACAGGCGGAAGCTGCGGGCCGCCTGGGTGGCCGGCGGGGCCCTCCTCACGCTGCTGCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrine Panoreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                583
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                                                                                                                       AW583167

443 bp mRNA linear EST 13-P
allfil., 14 Human Pancreatic Telete Homo sapiens CDNA clone
IMAGE: 5638029 5' similar to SW:GR40 HUMAN 014842 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR40. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washu-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                 AW583167.1 GI:7260111
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234 bp DNA linear GSS 24-SEP-2003 tigr-ges-dog-17000349748378 Dog Library Canis familiaris genomic, genomic survey sequence.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCC 441
                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                               322 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCCACGCCCCGGCTCCGTCTCACCCCT 381
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Kirkness, E. F., Bafna, V., Halpern, A. L., Levy, S., Remington, K., Rusch, D. B., Delcher, A. L., Pop, M., Wang, W., Fraser, C. M. and Venter, J. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 CTGAAAGCGGGGAGGCGCTAAGCTCCGGAACTCTGCCAGACTCGCCTGTGT
                                                                                                                                                                                                                                                                                             61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCT
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                                                                                                    Gaps
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
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                                 Score 295.2; DB 14; Length 609; Pred. No. 6.3e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AGTGCAGGCCGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCC 348
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                                                                                                 Indels
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                                                                                                 0; Mismatches 33;
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/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CE038975.1 GI:35069198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (dog)
                                 Query Match 32.7%;
Best Local Similarity 90.5%;
Matches 315; Conservative
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris
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| organism="Mono sapiens" |
| mol_type="mxna" |
| mol_type="mxna" |
| /mol_type="mxna" |
| /mol_type="mxna" |
| /issue_type="purified pancreatic islet" |
| /issue_type="purified pancreatic islet" |
| /ish host="bulds" |
| /lone | lib="HR85 islet" |
| /lone | lib="mxs |
| /l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1008c01.97 HRB5 islet Homo sapiens cDNA linear EST 03-DEC-2002 ipoBc01.97 HRB5 islet Homo sapiens cDNA clone IMAGE:6216192 5' similar to SW:GP40_HUMAN 014842 PUTATIVE G PROTEIN-COUPLED RECEPTOR CA776599
      240
                                                                                                                                                          GTCTTCGCGGTGGCCCACTTCTTCCCACTCTATGCCGGCGGGGCTTCCTGGCCGCCCTG 300
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I (bases 1 to 609)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Canfelsing, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tasgareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812

Pax: 617-495-8557

Ramail: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primm: -40Hp from Gibco
High quality sequence stop: 426.
   CTGAAGGCGGTGGAGGCGCTTCCGGGGCCTGGCCTCTGCCGGCCTCGCTGTGCCCC
                                                            Unpublished (2000)
Other ESTs: ip08c01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                             489 CGCTACTCCTGGGCCGTGTGTGCGCCCATATGGG 522
                                                                                                                                                                                                                                                                                                                                                                                    361 TGCTATTCCTGGGGGGGGGCGCCGCCATCTGGG 394
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Homo sapiens
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181
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE

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RESULT 8 CNS041EX

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CH230-339G19.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone BZ160914
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Blate: 339 row: G column: 19
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                                                                                                                                                                                                                                                                                                                                                       642 TCAACCTGTGCCTGGCCAACCTGGCCCTGGTGGCCTGGCTGCCGTCAAGGCCCTGGAGA 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Other_GSSs: CH230-339619.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                   522 TCGCTCTGGGCGTCTACGTCTTCACCTTCCTGCTGGCCTGCCGCCAACCTGCTGGTCC
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                                                         20 rerectresecerciangresecescritises
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
3; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
|mol_type="genomic DNA"
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252; Conservative
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561 bp DNA linear GSS 01-SEP-2000

Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
074E14 of library G from Tetraodon nigroviridis, genomic survey
                                 234 CCCTGGGCATCAACACGCCGGTCAACGGCTCTCCAGTCTGCCTGGAGGCCTGGGGACCCTG 175
                                                                                                                   589
                                                                                                                                               174 CCTCAGCGGGCCCCGCTCGCCCTCTCTCTCCTGCTCTTCTTCCTGCCCCTGACCA 115
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
CCCTGGGCATCAACACACCGGTCAACGGCTCTCCGGTCTGCCTGGAGGCCTGGGACCCGG 529
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                                                                                                                                                                                                                                                                     114 TCACGGCCTTCTGCTACGTGGGCTGCCTCCGGGCACTGGCCCCGCTCAGGCCACA 55
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Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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This sequence is a single read and was generated as part of a lar scale clone-and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                       TCACAGCCTTCTGCTACGTGGGCTGCCTCCGGGCACTGGCCCGGCTCCGGCCTGACGCACA
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/mol type="qenomic DNA"
/db xref="taxon:99883"
/clone="074E14"
/clone="074E14"
/clone lib="G"
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ALZ70114.1 GI:7992019
GSS; genome survey sequence.
Tetraodon nigroviridis
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BMS44968
AGENCOURT_6497637 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588752
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National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Righ quality sequence start: 26

High quality sequence start: 26

High quality sequence stop: 716.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1117)
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                                            Length 543;
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Pred. No. 1.3e-10;
0; Mismatches 317; Indels
                                                                                     Indels
                                                                                                                           1 ATGGACCTGCCCCCGCAGCTCTCCTTTCGGCCTCTATGTGGCCGCCT
                                         Score 128; DB 28;
Pred. No. 1.4e-12;
0; Mismatches 2;
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/organism="Homo sapiens"
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52.1%;
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Best Local Similarity 98.5%;
Matches 128; Conservative
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ119988 543 bp DNA linear GSS 22-SEP-1998 HS_3024_Al_H01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=1 Row=0, genomic survey
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
             /gex="Female"
/cell_type="Brain"
/coll_type="Brain"
/clone_lib="CHOR1-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHOR1-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Plate: 3024 row: O column: 1
Class: BAC ends
                                                                                                                                                                                                                              60; Indels
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|mol_type="genomic DNA"
|db xref="taxon:9606"
|clone="plate=3024 Col=1 Row=O"
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Location/Qualifiers
/clone="CH230-339G19"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 779)
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CATCCGAGGCGCGACGGCCCACGCCCGGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT
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National Institutes of Health, Mammalian Gene Collection
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/note="Vector: power_lay; Site 1: loxP-Sall; Site 2: loxP-HindII; Clones from this library have been loxP-HindIII; Clones from this library have been complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is CDNA derived from either pooled cytoplasmic polya RNA from 30 cells lines or pooled cytoplasmic polya RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Prederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at this is a NIH_MGC Library."
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11.8%; Score 106.6; DB 14; Length
al Similarity 51.0%; Pred. No. 9.2e-09;
343; Conservative 0; Mismatches 309; Indels
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/clone_lib="NIH_MGC_195"
Cound through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                   1. .779
/organism="Homo sapiens"
                                               http://image.llnl.gov
Plate: IRBK1 row: e column: 10
High quality sequence stop: 748.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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1 (bases 1 to 472)
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., White, J., Cho, J., Fahrenkrug, S. C., Casas, E., Mhite, J., Cho, W. W., Rohrer, G. A., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                     138 GAACCTGGGCTGCTGCTGCTGCTGACAGTCTCTCTGCCCCTGAAGGCGGTGGAGGC 197
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/clone_lib="WARC_1BOV"
/note="Vector: pCMV_SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from lymph node, ovary,
                                                                                                                                                                                                                                             CTTCTTCCCACTCTATGCCGGCGGGGGCTTCCTGGCCGCCCTGAGTGCAGGCCGCTACCT
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
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Seq primer: ATTTAGGTGACACTATAG.
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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFS were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-ECORV-XmnI/XhoI-3', 5'-ECORV-XmnI/XhoI-3', 5'-ECORV-XmnI/XhoI-3', please visit our anonymous ftp site at please visit our anonymous ftp site at ftp://image.lnh.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Rammalia, Buthoria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / MIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: IRBI02 row: f column: 12
High quality sequence stop: 680.
                                                                              618 CCGGGCACTGGCCCGCCTCACGCACAGGCGGAAGCTGCGGGCCGCCTGGGTGGC
                                                                                                                                 641 GTGGATCCTCGGCAGAGGGGAGCCACCGCCGGCAGAGGAGGAGGTGGCGGGCTGTTGGC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_14740239 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971953 5', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGB:6971953"
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Search completed: April 30, 2004, 16:32:52 Job time : 2953 secs
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Budocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Dr. Hiroshi Inoue
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Unpublished (2000)

Other Ests: ipo2f08.x1
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                                                                         Length 472;
                                                                      11.4%; Score 102.8; DB 12; Length llarity 53.8%; Pred. No. 3.7e-08; Conservative 0; Mismatches 182; Indels
Eat, hypothalamus, and pituitary."
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Seg primer: -40RP from Gibco
High quality seguence stop: 64.
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KEYWORDS
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/clone lib="MRB5 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not!; Site_2: Xho!; CDNA made by oligo-dr priming.
Size-selected on agarose gel. Average insert size -lkb. 5.
Xho! site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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/tissue type="Purified pancreatic islet"
/lab_host="DH108"
organism="Homo sapiens"
                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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Sequence 253, App
Sequence 273, App
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                                                                      April 30, 2004, 07:54:59; Search time 90 Seconds (without alignments) 5568.007 Million cell updates/sec
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-120-496D-271

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US-09-170-496D-253

US-09-170-496D-273

US-09-170-496D-273

US-09-170-496D-173

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US-09-170-496D-257

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US-09-472-130A-3
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Listing first 45 summaries
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301 AGTGCAGGCGGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG

361 TGCTATTCCTGGGGGGTGTGCGCGCCCATCTGGGCCCTCGTCCTGTGTCACCTGGGTCTG 420

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| Patent No. 5942416
| GENERAL INFORMATION:
| APPLICANT: Bergsma, Derk
| APPLICANT: Genesh, Sathe
| APPLICANT: Mao, Joyce
| TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
| TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: 3
| ADDRESSE: SmithKline Beecham Corporation | STREET: 709 Swedeland Road | CITY: King of Prussia
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GENERAL INFORMATION:
PAPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
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Pred. No. 2.3e-176;
0; Mismatches 3;
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Best Local Similarity 99.7
Matches 900; Conservative
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; ORGANISM: Homo sapiens
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US-09-170-496D-271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BERGSMA, DERK
APPLICANT: SATHE, GANESH M.
APPLICANT: PUETTERER, WENDY
APPLICANT: MAO, JOYCE
TITLE OF INVENTION: cDNA CLONE HNFDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUPERATURE SISTEM: DOS SOFTWARE: FEASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/248,715 FILING DATE: US-09-FEB-1999 CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/820,521 FILING DATE: 19-MAR-1997 ATTOWNEY/AGENT INFORMATION: NAME: Prestia, Paul FREGISTRATION NUMBER: 23,031 FREGISTRATION NUMBER: 23,031 FREGISTRATION NUMBER: 23,031
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Patent No. 6207800
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030 GGÉCTATATCTGC 1042
                                                                                                                                                                                                                                                                                                                                                                                                       738 CAGCTTCCTGTAC 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.3
Matches 383; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610-407-0700
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CITY: Valley Forge
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-248-715-1
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                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-WAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Han, William T REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50011
TELECOMUNICATION INFORMATION:
TELEPRAK: 610-270-5219
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SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
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STRANDEDNESS: single
                                                     ZIP: 19406
COMPUTER READABLE FORM:
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                              COUNTRY:
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678 CGGCGGGGCCCTCCTCACGCTGCTCTGCGTAGGACCCTACAACGCCTCCAACGTGGC 737
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Pred. No. 5.2e-17;
0; Mismatches 326;
                                                                                                                                                     NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-50011-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-248-715-1
                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                           FILING DATE: 09-Feb-1999
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                         TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 383; Conservative
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SATHE, GANESH M.
FUETTERER, WENDY
MAO, JONE HAPDY20 THAT ENCODES
TITLE OF INVENTION: CDNA CLONE HUPDY20 THAT ENCODES
A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
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OPERATIVE SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09248715
Patent No. 6277960
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTER READABLE FORM:
MEDIUM TYPE: Diskette
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ZIP: 19482
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: Patentin version 3.1
SEQ ID NO 273
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Pred. No. 4.8e-16;
0; Mismatches 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 273, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.8%;
Matches 380; Conservative
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CRGANISM: Homo sapiens
US-09-170-496D-273
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US-09-170-496D-273
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Patent No. 655539

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
970 GGGGCCACGCTGCTCCTTGTCTGCTTTGGGCCCTACAACGTGTCCCATGTCGT 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCGCGGCCATCTGGGCCCTCGTCCTGTGTCACCTGGGTCTGGTTTTGGGTTGGAGGC 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTGGGCTTCCCGC
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                                                                                                     738 CAGCTTCCTGTAC 750
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; ORGANISM: Homo sapiens
US-09-170-496D-253
                                                                                                                                                                                                                                                            RESULT 6
US-09-170-496D-253
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                                      399 rácicaccasácregraccióccircraragácraáricragadagrácagacaa
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8 TGCCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCCGCCTTTGCGCTTGGGCTTCCCGCTCA
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; Sequence 1, Application US/09479130
; Patent No. 6436400;
GENERAL INVERATION:
APPLICANT: Xu, Wenfeng
; APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Poster, Donald C.
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
TITLE OF INVENTION: PRA4 (ZCHEMR2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics, Inc.
STREET: L201 Eastlake Avenue East
CITY: Seattle
STRATE: WA
ZIP.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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                                               COGGGCACTGGCCTCCGGCCTGACGCACAGGCGGAAAGCTGCGGGCCGCCTGGGTGGC 677
                                                                                                                                                621 GGTGTGGATCCTCGGCAGAGGGGGCAGCCACCCCGGCAGAGAGGGGTGAAGGGGCTGTT 680
                                                                                                                                                                                           678 CGGCGGGCCCTCCTCACGCTGCTCTGCGTAGGACCCTACAACGCCTCCAACGTGGC 737
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Patent No. 6111075

GENERAL INFORMATION:
APPLICANT: Xu, Wenfeng
APPLICANT: Yee, David P.
APPLICANT: Peternell, Scott R.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.4%; Score 84.6; DB 3;
Best Local Similarity 47.2%; Pred. No. 5.4e-09;
Matches 329; Conservative 0; Mismatches 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2ymcGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/POCKET NUMBER: 98-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence
LOCATION: 176...1330
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98102
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Pred. No. 5.4e-09;
0; Mismatches 359; Indels
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APPLICANT: Presnell, Scott R.
APPLICANT: Yee, David R.
APPLICANT: Yee, David R.
APPLICANT: Yee, David C.
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR PAR4
TITLE OF INVENTION: (ZCHEMR2)
TITLE OF INVENTION: (ZCHEMR2)
TITLE OF INVENTION (WABER: US/09/472,130A
CURRENT APPLICATION NUMBER: US 09/053,866
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASELSEQ for Windows Version 3.0
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GENERAL INFORMATION:
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Best Local Similarity 47.2%;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,130
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 98-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence LOCATION: 176...1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-479-130-1
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-(TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 GGACCGCTACCTGGCTGTGGCCCATCCCTTCCACTTCCACTTCCGGACCCTGAAGGC 410
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A PELICANT: Derk J. Bergsma, Catherine E. Ellis
APPLICANT: Derk J. Bergsma, Catherine E. Ellis
TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor
TITLE OF INVENTION: HUVCT36
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STRATE: PA
COUNTRY: USA
ZOUNTRY: USA
ZOUNTRY: READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 4; Length 1098;
Pred. No. 4.2e-08;
0; Mismatches 190; Indels
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERPECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/170,496D CURRENT FILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 225
LENGTH: 1098
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Best Local Similarity 51.8
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-170-496D-225
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US-08-724-974A-1
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                          990 CGGCCAGCGGCCGGCGCTACGGCCACGCGCTGAGGCTGACCGCAGTGGTGCTGGCCTCCG 1049
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Pred. No. 4.2e-08;
0; Mismatches 190; Indels
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US-09-170-496D-225
Sequence 225, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117, Application US/09170496D Patent No. 6555339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 117
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Best Local Similarity 51.8<sup>3</sup>
Matches 207; Conservative
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US-09-170-496D-117
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US-09-170-496D-117
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377 CATCCACCAGACGCTGGCCCCGGTGGTCTATGTTACCGTGCTGGTGGTGGGCTTCCCGGC 436
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Best Local Similarity 51.8%; Pred. No. 4.3e-08;
Matches 207; Conservative 0; Mismatches 190; Indels
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Fatent No. 6645726
GENERAL INFORMATION:
APPLICANT: Howard:
APPLICANT: Palyha, Oksana C.
APPLICANT: Palyha, Oksana C.
APPLICANT: Smith, Roy G.
APPLICANT: Tan, Carina P.
TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
TITLE OF INVENTION: CANINE BROWTH HORMONE SECRETAGOGUE
TITLE OF INVENTION: RECEPTOR
FILLING DATE: 2001-05-30
CURRENT FILLING DATE: 2001-05-30
PRIOR FILLING DATE: 1999-08-06
PRIOR FILLING DATE: 1999-08-06
PRIOR PLICATION NUMBER: 60/095,960
PRIOR PLICATION NUMBER: 1999-08-06
PRIOR PLICATION NUMBER: 1999-08-06
PRIOR PLICATION NUMBER: 1999-08-06
PRIOR PLICATION NUMBER: 1998-08-10
PRIOR PLICATION NUMBER: 1998-08-10
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      PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION WUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Petentin version 3.1
SEQ ID NO 26
LENGTH: 1697
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CRGANISM: Canis familiaris
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1050)
US-09-762-661A-1
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Homo sapiens
US-09-364-425B-26
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US-09-762-661A-1
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, I-Lin
APPLICANT: Liam, I-Lin
APPLICANT: Chen, Ruoping
TILE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Rece
FILE REFERENCE: Aren0047
CURRENT APPLICATION NUMBER: 08/09/364,425B
CURRENT APPLICATION NUMBER: 60/094,879
FRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
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51.8%; Pred. No.
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGS0022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
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; Sequence 26, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610 270 5090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear ANTI-SENSE: No
                                                                                                                                                                                        PILING DATE:
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            Length 1050;
Query Match 8.7%; Score 78.2; DB 4; Length 1 Best Local Similarity 47.9%; Pred. No. 9.7e-08; Matches 292; Conservative 0; Mismatches 309; Indels
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Job time : 93 secs
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April 30, 2004, 15:43:35; Search time 465 Seconds (without alignments) 8784.275 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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903
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ddy	4pp	A	11	ddy	Ap	A	dat	dd	ij	11	Æ	ďď∖	ddy
		249, A	474, 1	23904	., Appli	11, 1	9201,	24088,	53, 7	604, App	App.	Appl	5146,	173, 7	15, 7
	Description	Seguence 2	Sequence 4	Sequence 2	Sequence 1	Sequence 2	Sequence 9	Sequence 2	Sequence 2	Sequence 6	Sequence 1	Sequence 3	Sequence 2	Sequence 2	Sequence 5
SUMMARIES	g:	US-10-251-385-249	US-10-225-567A-474	US-10-029-386-22904	US-10-202-687-1	US-10-251-385-271	US-10-029-386-9201	US-10-029-386-24088	US-10-251-385-253	US-10-225-567A-604	US-10-203-539-1	US-10-203-539-3	US-10-029-386-25146	US-10-251-385-273	US-10-225-567A-515
		15	15	15	16	15	15	15	15	15	15	15	15	15	12
	% Query Match Length DB	903	903	903	903	903	550	960	1041	1041	1041	1041	1206	1041	4895
	& Query Match	100.0	100.0	100.0	100.0	99.5	17.1	13.5	13.5	13.5	13.5	13.5	13.5	13.1	9.4
	Score	903	903	903	903	898.2	154	121.8	121.8	121.8	121.8	121.8	121.8	118.6	84.6
	Result No.	-	7	e	4	ហ	9	7	80	6	10	11	12	13	14

Segmence 1, Appli	'n		225,			Sequence 25332, A	Ä	Ξ	25	25,	25,	a)	257,					N			Sequence 2, Appli	ď	361	$\alpha$	2	27	29	27		29,
US-10-187-049-1	US-09-850-948-5	US-10-251-385-117	US-10-251-385-225	US-10-273-575-5	US-10-225-567A-282	US-10-029-386-25332	US-10-109-533A-1	US-10-288-222A-11	US-09-853-161-25	US-09-852-659A-25	US-09-852-797-25	US-10-058-993-25	US-10-251-385-257	US-10-225-567A-466	US-10-337-992-1	US-10-029-386-25403	US-10-348-190-3	US-10-251-385-275	US-10-348-190-1	US-10-203-539-5	US-10-400-991-2	US-10-190-469-2	US-10-225-567A-361	US-09-254-783A-2	US-10-152-058-2	US-09-875-076-27	US-09-876-252-29	0-272-983	US-10-393-807-27	US-10-417-820A-29
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4895	1098	1098	1098	1098	1098	1434	1691	1691	1329	1329	1329	1329	993	993	993	994	1616	993	2426	960	1955	1955	1116	2427	2427	1080	1080	1080	1080	1080
4.6	8.9	8.9	8.9	8.9	8.9	8 .9	8.9	8.9	8.7	8.7	8.7	8.7	8.5	8.5	8.5	8.5	8.5	8.4	8.1	7.8	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	7.6
84.6	80	80	80	80	80	80	80	80	78.2	78.2	78.2	78.2	77.2	77.2	77.2	77.2	77.2	75.6	73.2	70.8	70.4	70.4	70	70	70	68.4	68.4	68.4	68.4	68.4
15	16	17	18	19	20	c 21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Sequence 249, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Law, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT FILING DATE: 2002-09-20
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SEQ ID NO 249
; SEQ ID NO 249
; SEQ ID NO 249 TYPE: DNA ORGANISM: Homo sapiens RESULT 1 US-10-251-385-249 US-10-251-385-249

Gaps ö Length 903; Indels Query Match
100.0%; Score 903; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-210;
Matches 903; Conservative 0; Mismatches 0;

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61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCACGCCCGGCTCCGTCTCACCCCT 120 9 1 ATGAACCTGCCCCCGCAGCTCTCCTTCGGCCTCTATGTGGCCGCCTTTGCGCTGGGCTTC 1 ATGGACCTGCCCCCCCCAGCTCTTCGGCCTCTATGTGGCCCGCCTTTGCGCTGGGCTTC 61 CCGCTCAACGTCCTGGCCATCCGAGGCGCGACGCCCCACGCCCCGGCTCCGTCTCACCCT В ઠે 8 8 ઠ

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121 AGCCTGGTCTACGCCCTGAACCTGGGCTGCTCCGACCTGCTGCTGACAGTCTCTCTGCCCC
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                                                                         100.0%; Score 903; DB 15;
100.0%; Pred. No. 3.8e-210;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 903; Conservative
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            ; LENGTH: 903
; TYPE: DNA
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US-10-225-567A-474

i Sequence 474. Application US/10225567A

j Publication No. US20030113798A1

j GENERAL INFORMATION:
   APPLICANT: LifeSpan Biosciences
   APPLICANT: Brown, Joseph P.
   APPLICANT: Burmer, Glenna C.
   APPLICANT: Roush, Christine L.
   TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
   FILE REFERENCE: 1920-4-4
   CURRENT FILING DATE: 2001-12-19
   PRIOR APPLICATION NUMBER: 60/257,144
   PRIOR PILING DATE: 2000-12-19
   NUMBER OF SEQ ID NOS: 2292

NUMBER OF SEQ ID NOS: 2292
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Sequence 1, Application US/10202687

Publication No. US20040019109A1

GENERAL INFORMATION:
APPLICANT: OWMAN, CHRISTER
APPLICANT: OLDE, BJORN
APPLICANT: OLDE, BJORN
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS AFFECTING FATTY ACID
TITLE OF INVENTION: METABOLISM
TITLE OF INVENTION: METABOLISM
FILE REFERENCE: 07675.0007 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/202,687
CURRENT FILING DATE: 2002-07-24
NUMBER OF SEQ ID NOS: 4
SOFFWARE: PATECHIN OF: 2.1
SEQ ID NO
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ORGANISM: Homo sapiens
US-10-202-687-1
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                                                     Sequence 22904, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Hondan GCOMBED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 22904
LENGTH: 903
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OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: NT HIT: gill526068, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: 014842, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AM583167.1, EVALUE 0.00e+00

US-10-029-386-22904
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100.0%; Pred. No. 3.8e-210;
tive 0; Mismatches 0;
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Best Local Similarity
                   RESULT 3
US-10-029-386-22904
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Oy 301 AGTGCAGGCGGCTACCTGGGAGCAGCCTTCCCCTTGGGCTACCAAGCCTTCCGGAGGCCG 360	0y 361 IGCTATTCCTGGGGGGTGTGCGCGCATCTGGGCCTCGTCCTGTGTCACCTGGGTCTG 420	Qy         421         GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGCTGGAACCACAGCAACACCTCCCTGGGCATC         480           Db         421         GTCTTTGGGTTGGAGGCTCCAGGAGGCTGGCTGGCTGGACCACAGCAACCTCCCTGGGCATC         480	QY         481         AACACACCGGTCAACGGCTCTCCGGTCTGCAGGCCTGGAACCCGGCCTTGCCGGC         540           Db         481         AACACACCGGTCAACGGCTCTCCGGTCTGCAGGGCCTGGAGGCCTCGGCCTCTGCCGGC         540	Qy 541 CCGGCCCGCTTCAGCCTCTCTCTGCTCTTTTTCTGCCCTTGGCCATCACAGCCTTC 600	Qy         601         TGCTACGTGCCTGCCTCCGGCACTGGCCTCCGGCCTGACGCACAGGGGAAGCTG         660           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         661         CGGGCCCCTGGGTGGCCGGGGGCCCTCCTCA.CGCTGCTGCTTGCGTAGGACCCTAC         720           Db         661         CGGGCCGCTGGGTGGCCGGGGGCCCTCCTCA.CGCTGCTGCTGCTTGCGTAGGACCCTAC         720	Qy         721         AACGCCTCCAACGTGGCCAGCTTCCTGTACCCCAATCTAGGAGGTCCTGGCGGAAGCTG         780           Db         721         AACGCCTCCAACGTGCCCAGCTTCCTGTACCCCAATCTAGGAGGTCCTGGCGGAAGCTG         780	Qy         781         GGGCTCATCACGGGTGCCTGGAGTGTGCTTAATCCGCTGACCGGTTACTTGGGA 840           Db         781         GGGCTCATCACGGGTGCCTGGTGCTTAATCCGCTGGTGACCGGTTACTTGGGA 840	QY 841 AGGGGTCCTGGCCTGAAGACAGTGTGCGCCAAGAACGCAAGAGGGGCAAGTCCCAGAAG 900	Qy         901 TAA 903           Db         901 TAA 903	RESULT 5 US-10-251-385-271	; Sequence 271, Application US/1U251385 ; Publication No. US20030105292A1 ; GENERAL INFORMATION: ; APPLICANT: Behan, Dominic P.	<pre>; APPLICANT: Chalmers, Derek T. ; APPLICANT: Liaw, Chen W. ; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human; ; TITLE OF INVENTION: Protein-Coupled</pre>	; TITLE OF INVENTION: Receptors ; FILE REFERENCE: AREN-040 ; CURRENT APPLICATION NUMBER: US/10/251,385 ; CURRENT FILING DATE: 2002-09-20	; PRIOR APPLICATION NUMBER: US/09/170,496 ; PRIOR FILING DATE: 1998-10-13 ; NUMBER OF SEQ ID NOS: 294	; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 271 ; LENGTH: 903	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-251-385-271	Query Match 99.5%; Score 898.2; DB 15; Length 903; Best Local Similarity 99.7%; Pred. No. 5.6e-209; Matches 900; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Sequence 253, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Behan, Dominic P.
    APPLICANT: Law, Chen W.
    TITLE OF INVENTION: Protein-Coupled
    TITLE OF INVENTION IN
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                                        CATCCGAGGCGCGACGCCCACGCCCGGCTCCTCACCCCTAGCCTGGTCTACGCCCT
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; ORGANISM: Homo sapiens
US-10-251-385-253
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRENCE: ACOUNTGA.*2.
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24088
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REPERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
OTHER INFORMATION: SMISSPROT HIT: 0.4842, EVALUE 1.00e-22
OTHER INFORMATION: ST HUMAN HIT: AU117321.1, EVALUE 2.00e-01
OTHER INFORMATION: NT HIT: U62631.1, EVALUE 0.00e+00
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EXPRESSED IN HELA, SIGNAL = 2.7

EXPRESSED IN BRAIN, SIGNAL = 1.7

EXPRESSED IN HEART, SIGNAL = 1.5

EXPRESSED IN HEART, SIGNAL = 1.5

EXPRESSED IN HEART O1529, EVALUE 0.00e+00

NT HIT: AF024689.1, EVALUE 0.00e+00

EST_HUMAN HIT: AA860692.1, EVALUE 2.20e-02
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Pred. No. 2.5e-20;
0; Mismatches 327; Indels
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Pred. No. 3.9e-28;
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Best Local Similarity 52.1
Matches 382; Conservative
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ORGANISM: Homo sapiens
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US-10-029-386-24088
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                                                                                                                                                                                                                                               Score 121.8; DB 1
Pred. No. 2.5e-20;
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Publication No. US20030113810A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USW
                                                                                                                                                                                                                                               13.5%;
52.1%;
                            SOFTWARE: Patentin version 3.1 SEQ ID NO 604
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Matches 382; Conservative
NUMBER OF SEQ ID NOS: 2292
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                                                                                                                      TYPE: DNA
CRGANISM: Homo
US-10-225-567A-604
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APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 2001-12-19
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                                                                                                                                                                                                                                                                               CATCCGAGGCGCGACGCCCACGCTCCGTCTCACCCCTAGCCTGGTCTACGCCCT 137
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                               DB 15; Length 1041;
                                                                                            0; Mismatches 327; Indels
                               Score 121.8; DB 1
Pred. No. 2.5e-20;
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APPLICANT: LifeSpan Biosciences
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52.1%;
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US-10-225-567A-604
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                                   Query Match
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285 CTTCACCACCATCTATCTCACCGCCCTCTTCCTGGCAGCTGTGAGCATTGAACGCTTCCT 344
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Pred. No. 2.5e-20;
0; Mismatches 327;
                                                                      RESULT 11
US-10-203-539-3
Sequence 3, Application US/10203539
Sequence 3, Application US/10203539
Sequence 3, Application US/10203539
Sequence 3, Application No. US20030113810A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USW
CURRENT APPLICATION NUMBER: US/10/203,539
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: GB 0003900.8
FRIOR FILING DATE: 2000-03-18
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 3.0
SOFTWARE: Patentin Ver. 3.0
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13.5%;
Best Local Similarity 52.1%;
Matches 382; Conservative
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ORGANISM: Homo Sapiens
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Pred. No. 2.5e-20;
0; Mismatches 327; Indels
CURRENT APPLICATION NUMBER: US/10/203,539
CURRENT FILING DATE: 2002-08-09
FRIOR APPLICATION NUMBER: GB 0003900.8
FRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO.1
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Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fanh, David R.
APPLICANT: Fanh, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HAZEL, DAVID RECOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR UTILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 25146
LENGTH: 1206
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52.1%; Pred. No. 2.4e-20;
tive 0; Mismatches 327; Indels 24;
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OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXT HUMAN HIT: BF115946.1, EVALUE 2.80e-02

OTHER INFORMATION: SWISSPROT HIT: O14843, EVALUE 0.00e+00

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								RECEPTORS					<u> </u>		
378 GTGCGCGGCCTTGGGCCCTCGTCTCTCTCTCTGGTCTTTGGGTTGGAGGC 437	465 CTCAGGGGACATCTCCCACAGGCACCAATGGGACCTG 506 498 CTCTCCGGCTCTGCAGGCCTGGAACCCGCCCCGCCCGCCC	CTCTCTCCTGCTCTTTTTTTCTGCCCTTGGCGATCACAGCCTTCTGCTAGGCTGCCGTGCCCTTGCTGCTAGGCCTTCTGCTAGTGCCTTGCTGCTAGTGCCTTGCTAGTGCTGCTTGCT					-10-22-36-A-39 Sequence 515, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION: APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.	AFFLICANT: BOLLMET, CALEBING C. TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RI FILE REFERENCE: 1920-4-4 CURRENT APPLICATION NUMBER: US/10/225,567A	TFILING DATE: 2001-12-19 APPLICATION NUMBER: 60/257,144 FILING DATE: 2000-12-19 ? OF SEQ ID NOS: 2292 RRE: Patentin version 3.1	SEQ ID NO 515 LENGTH: 4895 TYPE: DNA ORGANISM: Homo sapiens	-10-225-567A-515 Query Match Query Match Best Local Similarity 47.2%; Pred. No. 2.4e-11; Matches 329; Conservative 0; Mismatches 359; Indels 9; Gaps 2;	8 IGCCCCGCAGCTCTCCGCCTCTAIGTGGCCCCCTTTGCGCTGGGCTTCCCGCTCA 67	68 ACGTCCTGGCCATCCGAGGCGCAGACCCCCCCCCCCTCCTCACCCCTAGCCTGG 127	128 TCTACGCCCTGAACCTGGGCTGCTGCCGACCTGCTGCTGACGCTCTCTGCCCCTGAAGG 187	188 CGGTGGAGGCCTACCCTCCGGGGCCTGGCGGCTCGCTGTGCCCGTCTTCG 247

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Job time : 468 secs
LENGTH: 4895 base pairs
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AAY15082
AAY45036
AAB47623
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                                                            AAG79597
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 April 29, 2004, 12:03:33 ; Search time 59 Seconds (without alignments) 1436.682 Million cell updates/sec
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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                1586107 segs, 282547505 residues
                          protein search, using sw model
                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                     seq length: 0
seq length: 200000000
                                                          US-10-202-687-2
1584
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Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

## ALIGNMENTS

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (ICS) and transmembrane domain 6 (TMG). A non-endogenous maino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-AAA15-Pro. The endogenous amino acid is selected from Ly9, His, Arg or AAA15-Pro. The endogenous amino acid is selected from Ly9, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical Example 1; Page 308-309; 341pp; English. Human G protein-coupled receptor GPR40 AAY90679 standard; protein; 300 AA. 3 Liaw 99WO-US023938 98US-00170496 (first entry) Chalmers DT, (AREN-) ARENA PHARM INC WPI; 2000-329165/28. N-PSDB; AAA30759. WO200022129-A1. Homo sapiens. 12-OCT-1999; 13-OCT-1998; 21-AUG-2000 20-APR-2000. antagonist. Behan DP, AAY90679; agents. RESULT 1 AAY90679 Aay90679 Human G p
Abg31106 Human G p
Abg81994 Human G p
Adb61404 Human G p
Adb61404 Human G p
Ady20684 Human mut
Adc22791 Human G p
Adb61416 Monkey GP
Abg31107 Mouse G p
Adb61400 Mouse G p Rat GPR40
Hameter G
Human G-p
Human G-p
Human G P
Human G P
Human T-t
Human 7-t
Human G P
Human 7-t
Human G P
Human G P
Human G P
Human Human G P Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description Ady90684
Adc22791
Adc22791
Adc31107
Adb61406
Adb61402
Adb61402
Adb61402
Adb61402
Adb82759
Adb82759
Adb82759
Adx292773
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Adx99689
Adx99689 SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries ABG31106
ABP81994
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ADC22791
ADB614107
ADB614107
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geneseqp1980s:\*
geneseqp200s:\*
geneseqp2001s:\*
geneseqp2001s:\*
geneseqp2003s:\* geneseqp2004s:\* 80 Length 3346 3346 3330 3330 3330 Query Match 100.0 23.1

Result

Database

amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. The present sequence represents a human wild-type GPCR referred to in an exemplification of the invention 8 $\pm$ 8

Sequence 300 AA;

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240 61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 241 NASNVASFLYPNLGGSWRKLGLITGAMSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 9 9 1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLP 181 PARFSLSLLLFFLPLATTAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP Gaps ; 0 100.0%; Score 1584; DB 3; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Indels 0 Query Match Best Local Similarity 100. Matches 300; Conservative 181 121 121 8 g ઠે 셤 à 셤 ò 셤 ð ద

ABG31106 standard; protein; 300 AA (first entry) 21-OCT-2002 ABG31106; ABG31106

ID ABG3

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AC ABG3

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DT 21-0

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KW G pr

KW G Pr

KW G Pr

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HOWO

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PN WO20

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XX

XX

XX

XX

NY

PN WO10

PN WO10 RESULT

Human G protein-coupled receptor GPR40.

Human, GPR40, G protein-coupled, receptor, type 2 diabetes, obesity, antidiabetic, neuroprotective, anorectic, cerobroprotective, Gq; G protein, reporter gene, glucose intolerance, insulin intolerance, neurodegenerative disease; Alzheimer's disease; stroke.

Homo sapiens,

WO200257783-A2

25-JUL-2002.

18-DEC-2001; 2001WO-US048985 22-DEC-2000; 2000GB-00031527 (GLAX ) GLAXO GROUP LTD. (SMIK ) SMITHKLINE BEECHAM PLC.

Tadayyon M; Sauls HR, Muir AI, ¥, Ignar Andrews JL, Briscoe CP,

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; grotein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; ADDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; esteoporosis; cardiomyopathy; inflammation; crohn; disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

Human G protein-coupled receptor GPR40 protein SEQ ID NO:475.

WPI; 2002-599726/64. N-PSDB; ABK90236.

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the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecting whether the test compound competitively inhibits the binding of a farty acid GPR40 ligand to a GPR40 erceptor. Also included comprises detecting whether the test compound competitively inhibits the binding of a farty acid GPR40 ligand to a GPR40 erceptor. Also included comprising: (a) measuring any detectable signal produced by a reporter gene (comprising: (a) measuring any detectable signal produced by a reporter comprising a reporter gene under the control of G protein Gq cresponsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist, or (c) detecting whether the compound decreases glucose-stimulated insulin release from mammalian pancreatic beta cells in the presence of a GPR40 agonist, compared to glucose-stimulated insulin release that would occur cdue to the presence of the GPR40 agonist (2) a method of screening any compound for GPR40 agonist activity, which comprises: (a) detecting any compound for GPR40 agonist activity, which comprises: (a) detecting any compound for GPR40 agonist activity, which comprises: (b) detecting whether the compound binds to GPR40 and increases glucose-stimulated insulin release from mammalian cantagonist or agonist compounds for treating disorders e.g. type 2 antagonist or agonist compounds for treating disorders e.g. type 2 disabase (e.g. Alzheimer's disease) or stroke. The present sequence represents human GPR40
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Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor.
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                                                                                                                                           The invention relates to screening a test compound to determine whether
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                                                                                             Disclosure, Page 48-49; 53pp; English.
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Matches 300; Conservative
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mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                     (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                  19-DEC-2001; 2001WO-US050107
                                                           19-DEC-2000; 2000US-0257144P
                                                                               Roush CL,
                                                                                         WPI; 2003-046718/04.
                                                                                              N-PSDB; ABZ42843.
                             WO200261087-A2
                    Homo sapiens.
                                        08-AUG-2002
                                                                               Burmer GC,
          ulcer.
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure, Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polyapptide in a sample; and (2) an isolated antibody having high specificity and high affinity or cardidate polyapptide in a sample; and (2) an isolated antibody having high specificity and high affinity or antibody against a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for captaing immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzhaimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, disease, variation, sectoporosis, cancer, cardiomyopathy, chronic and acute disease, parkinson's disease, multiple sclerosis, pain, psoriasis, canxety, depression, schizophrenia, dementia, memory conservation, renal disorders, rheumatoid arthritis, trauma, ulcers, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or way the present invention inmunoassays and immunodiagnosis. Abs21523 to ABS21869 encode GPCR proteins given in ABPB1675 to ABBP2018, which are used in the

Sequence 300 AA;

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LKAVEALASGAWPLPASLCPVFAVAHFPPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                         61 LKAVEALASGAMPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFPLGYQAFRRP 120
                                                                                                                                                                                                                                CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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100.0%; Score 1584; DB 6; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Indels 0
                                       Matches 300; Conservative
                     Local Similarity
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181 PARFSLSLLLEFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240

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241 NASNVASFLYPNLGGSWRKLGLITGAMSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 셤 ò

RESULT 4 ADB61404

ADB61404 standard; protein; 300 AA

ADB61404;

04-DEC-2003 (first entry)

Human GPR40 protein.

fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; ophthalmological; antilipaemic; dermatological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; noctropic; anorectic; hypotensive; cytostatic; diabetic; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; bone diabetic retinopathy; hyporlipaemia; skin disease; arthritis; bone disease; arteriosclerosis; thrombosis; hypotratios; nocion; memory loss; obesity; hypoglycaemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; human.

Homo sapiens.

WO2003068959-A1.

21-AUG-2003.

13-FEB-2003; 2003WO-JP001483

14-FEB-2002; 2002JP-00037131. 12-JUL-2002; 2002JP-00204163. 12-NOV-2002; 2002JP-00328696.

22-JAN-2003; 2003JP-00014032 

(TAKE ) TAKEDA CHEM IND LTD

Ito Y, Kobayashi M, Tanaka H, Okubo S; Kawamata Y, Ogi K, Harada M, Fukusumi S; Hosoya M, Kizawa H, o, Pujii R, Hinuma

WPI; 2003-671661/63. N-PSDB; ADB61403. Fatty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.

Claim 34; Page 235-236; 257pp; Japanese.

and eicosanoid-binding G-protein complete receptor protein, GPR40,

coriginating in mouse, rat, crab-earing machey and hamater (sequences

fully defined in the specification), equivalent proteins of smilar

activity, and peptides containing partial sequences of the GPR40 protein.

The novel fatty acid and GPR40 protein and their compositions have the

following activities: antidiabetic, anabolic, neuroprotective,

nephrotropic, ophthalmological, antilipaemic, dermatological,

notropic, ancectic, hypotensive, and cytostatic. The novel fatty acid

and eicosanoid-binding G-protein coupled receptor protein, GPR40, and

curther compositions can be used in the treatment, prevention and

diagnosis of diabetes, ketosis, diabetic neuropathy, diabetic

curther compositions are not in acidosis, diabetic neuropathy, diabetic

arthritis, bone diseases, arteriosolerosis, thrombosis, hypertension,

indigestion, memory loss, obesity, hyporlipaemia, skin diseases,

indigestion, memory loss, obesity, hyposilycaemia, edema, innulin

resistance, insulin allergy, fat metabolism disorders and cancer. This

sequence represents a human GPR40 protein of the invention. The invention relates to a novel screening method comprising a fatty acid

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Synthetic.
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                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                                                                                                              CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARFSLSLLFFLPLAITAFCTVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                     MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                   LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP
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                                                                                              Gaps
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                                       100.0%; Score 1584; DB 7; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G protein-coupled receptor (GPCR) polypeptide #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 250; 221pp; English
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98US-00060188.
98US-0090783P.
98US-0095677P.
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                                                                                           Matches 300; Conservative
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N-PSDB; ADC22768.
                                                                  Local Similarity
Sequence 300 AA
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26-JUN-1998;
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                                               Query Match
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version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR polypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR. The method allows screening for compounds that modulate the activity of a human G protein-coupled receptor without the need for provision of a ligand for the receptor. This is particularly useful in allowing screening of compounds against orphan receptors for which no ligand is currently known. This sequence represents a human GPCR polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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intracellular loop 3; transmembrane domain 6; drug screening; agonist;
antagonist; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1584; DB 7; Length 300; 100.0%; Pred. No. 1.6e-149; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY90684 standard; protein; 300
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Matches 300; Conservative
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N-PSDB; AAA30776.
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29-APR-2003

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AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743) and tanamembrane domain 6 (TW6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acid N-terminal of an endogenous proline in TW6 to form a sequence X-caids N-terminal of an endogenous proline in TW6 to form a sequence X-da, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous can endogenous and non-endogenous can anixture of endogenous and non-endogenous candomists are also useful for treating for anixtogenists are also useful for treating diseased and disorders associated with that receptors in normal and diseased conditions. Anixagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAY90643-
                                                                                                                                                                                                         constitutively active, non-endogenous versions
Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                     Example 2; Page 325-326; 341pp; English.
                                                                                                                                                                                                      The invention relates to
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Sequence 300 AA;

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61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFLGYQAFRRP 120
                                                                                                                                                        CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                          PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                  181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAKWVAGGALLTLLLCVGPY 240
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                                                                    1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                       MDLPPQLSFGLYVAAFALGFPLAVTAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
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Length 300;
                                   1; Indels
99.7%; Score 1579; DB 3; 99.7%; Pred. No. 5.1e-149; iive 0; Mismatches 1;
                                   Matches 299; Conservative
                   Local Similarity
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Human G protein-coupled receptor (GPCR) polypeptide #76.
            ADC22791 standard; protein; 300 AA
                                       18-DEC-2003 (first entry)
                          ADC22791;
     RESULT 7
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Human, G protein-coupled receptor, GPCR, transmembrane-6 region, TM6, intracellular-3 region, IC3, receptor.

240

240

180

9

Homo sapiens

US6555339-B1

ADB61416 standard; protein; 300 AA

ADB61416 ID ADB6 RESULT 8

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The invention relates to a method for treating a non-endogenous, constitutively active version of an endogenous human G protein-coupled receptor (GPCR) that has a transmembrane-6 (TMG) region and an intracellular-3 (IC3) region, by substituting a specific amino acid in intracellular-3 (IC3) region, by substituting a specific amino acid in the TMG region with a different amino acid, and testing for constitutive activity. The method is useful for creating a constitutively active version of an endogenous human GPCR that comprises a transmembrane 6 region and an intracellular loop 3 region. The altered human GPCR copypeptides are useful for screening test compounds for identification of inverse agonists or partial agonists of GPCR polypeptides, which may have therapeutic uses. The altered GPCRs may also be used in vivo or in vitro in biological research. A nucleic acid encoding the altered GPCR may be used to create a transgenic animal expressing the altered GPCR conting of compounds for compounds that modulate the activity of a ligand for the receptor. This is particularly useful in allowing currently known. This sequence represents a human GPCR polypeptide of the
                                                                                                                                                                                                                                                                                                                              Creating a constitutively active version of an endogenous human G protein coupled receptor (GPCR) comprises substituting a specific amino acid in the transmembrane-6 region with a different amino acid, and testing for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 272; 221pp; English.
                                                                                                                                                                                                                           Chalmers DT;
                                                                                                  98US-00060188.
98US-0090783P.
                                        98US-00170496
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Best Local Similarity 99.7
Matches 299; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          constitutive activity
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26-JUN-1998;
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Monkey GPR40 04-DEC-2003 Fujii R, ADB61416; 

fatty acid; eicosanoid-binding G-protein coupled receptor; GPR40; antidiabetic; anabolic; neuroprotective; nephrotropic; opthalmological; antilipaemic; dermatological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetic retinopathy; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; bone disease; arteriosclerosis; thrombosis; hypotension; indigestion; memory loss; obesity; hypoglycemia; edema; insulin resistance; insulin allergy; fat metabolism disorder; cancer; monkey. Ito Y, Kobayashi M, Tanaka H, Okubo S Kawamata Y, Ogi K, Harada M, Fukusumi 14-FEB-2002; 2002JP-00037131. 12-JUL-2002; 2002JP-00204163. 12-NOV-2002; 2002JP-00326596. 22-JAN-2003; 2003JP-00014032. 13-FEB-2003; 2003WO-JP001483 (TAKE ) TAKEDA CHEM IND LTD Новоуа М, Kizawa H, WPI; 2003-671661/63 N-PSDB; ADB61417. WO2003068959-A1 21-AUG-2003. Hinuma S, Primates.

Fatty acid and eicosanoid-binding G-protein coupled receptor protein GPR40 for control of pancreatic function and treatment of diabetes.

Claim 1; Page 240-241; 257pp; Japanese.

The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and eicosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamater (sequences fully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and thehair compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarterisoclarotic, antiarthritic, osteopathic, thrombolytic, nootropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and clarence compositions can be used in the treatment, prevention and diagnosis of diabetic retinopathy, hyperlipaemia, skin diaesses, capturitis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hyposlycaemia, edema, insulin allergy, fat metabolism disorders and cancer. This sequence represents a monkey GPR40 protein of the invention.

Sequence 300 AA;

Gaps ö Length 300; 10; Indels Score 1519; DB 7; Pred. No. 4.9e-143; 0; Mismatches 10; DB 7; Query Match
Best Local Similarity 96.7%;
Matches 290; Conservative

61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120

1 MDLPPQLSFALYVAAFALGFPLNVLAIRGARAHARRRLTPSLVYALNLGCSDLLLTVSLP MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP

> 셤 ò

9

> ò 셤 8 셤 ò 셤

(first entry)

protein.

ABG31107 standard; protein; 300 AA. RESULT 9 ABG31107

ABG31107;

(first entry 21-OCT-2002 Mouse G protein-coupled receptor GPR40.

Mouse; GPR40; G protein-coupled; receptor; type 2 diabetes; obesity; antidiabetic; neuroprotective, antectic; cerobroprotective; Gq; g protein; reporter gene; glucose intolerance; insulin intolerance; neurodegenerative disease; Alzheimer's disease; stroke. 

WO200257783-A2

25-JUL-2002.

18-DEC-2001; 2001WO-US048985.

22-DEC-2000; 2000GB-00031527.

SMIK ) SMITHKLINE BEECHAM PLC. GLAX ) GLAXO GROUP LID.

Ignar DM, Muir AI, Sauls HR, Tadayyon M; Andrews JL, Briscoe CP,

WPI; 2002-599726/64. N-PSDB; ABK90237.

Identifying GPR40 receptor ligand for treating disorders e.g. obesity, comprises detecting whether the test compound competitively inhibits the binding of a fatty acid GPR40 ligand to a GPR40 receptor.

Disclosure, Page 51; 53pp; English.

The invention relates to screening a test compound to determine whether the compound is a GPR40 receptor (G protein-coupled receptor) ligand comprises detecting whether the test compound competitively inhibits the binding of a farty acid GPR40 ligand to a GPR40 receptor. Also included comprising: (a) measuring any detectable signal produced by a reporter comprising; (a) measuring any detectable signal produced by a reporter gene (comprising) a reporter gene under the control of G protein Gq responsive transcriptional element); (b) detecting a decrease in reporter gene expression in the presence of both test compound and agonist; or (c) detecting whether the compound and agonist; or (c) detecting whether the compound and agonist; or (c) detecting whether the GPR40 agonist; (2) a method of screening a compound for GPR40 agonist; (2) a method of screening a compound for GPR40 agonist; (2) a method of screening a compound for GPR40 agonist activity, which comprises: (a) detecting any reporter gene expression; or (b) detecting whether the compound binds to GPR40 and increases glucose-stimulated insulin release from mammalian pancreatic beta cells. The method is useful for identifying GPR40 antagonist or agonist compounds for treating disorders e.g. type 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LKAVEALASGAWPLPLPFCPVFALAHFAPLYAGGGFLAALSAGRYLGAAFPFGYQAIRRP 120
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diabetes, obesity, glucose or insulin intolerance, neurodegenerative disease (e.g. Alzheimer's disease) or stroke. The present sequence represents mouse GPR40
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                                                                                                                                                                                             Length 300,
                                                                                                                                                                                                                                                             17; Mismatches 34; Indels
                                                                                                                                                                                             84.2%; Score 1333; DB 5;
83.0%; Pred. No. 1.8e-124;
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12-JUL-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
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                                                                                                                                    Sequence 300 AA;
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The invention relates to a novel screening method comprising a fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences tully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antilipaemic, dermatological, antiarterioscherotic, antiarthritic, osteopathic, thrombolytic, nootropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and eicosanoid-binding G-protein coupled receptor protein, GPR40, and diagnosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyporlipaemia, skin diseases, arthritis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin cresistance, insulin allergy, fat metabolism disorders and cancer. This sequence represents a mouse GPR40 protein of the invention.
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GPR40 for control of pancreatic function and treatment of diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 1333; DB 7;
83.0%; Pred. No. 1.8e-124;
ive 17; Mismatches 34;
                                         Claim 1; Page 230-231; 257pp; Japanese.
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WO2003068959-A1

Fatty acid and eicosanoid-binding G-protein coupled receptor protein

, Okubo S; Fukusumi S

, Tanaka H, Harada M, B

Kobayashi M, Y, Ogi K, H

Kawamata

Hosoya M, Kizawa H,

Hinuma S,

Pujii R,

2003-671661/63

WPI; 2003-671661/ N-PSDB; ADB61401

Ito Y,

(TAKE ) TAKEDA CHEM IND LTD

ADB61428;

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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, originating in mouse, rat, crab-eating monkey and hamster (sequences cully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and theat compositions have the collowing activities: antidiabetic, anabolic, neuroprotective, nephrotropic, ophthalmological, antidiabetic, anabolic, neuroprotective, nephrotropic, antiatrhitic; osteopathic, thrombolytic, notropic, antiatrhitic, osteopathic, thrombolytic, and elcosanoid-binding G-protein coupled receptor protein, GPR40, and elcosanoid-binding G-protein coupled receptor protein, GPR40, and functions can be used in the treatment, prevention and funganosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic retinopathy, hyperlipaemia, skin diseases, arthitis, bone diseases, arteriosclerosis, thrombosis, hypertension, arthitis, bone diseases, arteriosclerosis, thrombosis, hypertension, resistance, insulin allersy, fat metabolism disorders and cancer. This sequence represents a rat GPR40 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
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Fukusumi S;
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81.7%; Pred. No. 3.6e-123;
ive 19; Mismatches 36; Indels
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                                                                                                                                                                                                                                          , Tanaka H
Harada M,
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Kawamata Y, Ogi K, F
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                                                                                                  14-FEB-2002; 2002JP-00037131.
12-JU-2002; 2002JP-00204163.
12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
                                                          13-FEB-2003; 2003WO-JP001483
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Best Local Similarity 81.7%
Matches 245; Conservative
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Kizawa H,
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N-PSDB; ADB61403.
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The invention relates to a novel screening method comprising a fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, coriginating in mouse, rat, crab-eating monkey and hamster (sequences tully defined in the specification), equivalent proteins of similar activity, and peptides containing partial sequences of the GPR40 protein. The novel fatty acid and GPR40 protein and their compositions have the following activities: antidiabetic, anabolic, neuroprotective, comprortoric, ophthalmological, antilipaemic, dermatological, antiarterisoslerotic, antiarthritic, ossteopathic, thrombolytic, concropic, anorectic, hypotensive, and cytostatic. The novel fatty acid and elcosanoid-binding G-protein coupled receptor protein, GPR40, and curropic, and elcosanoid-binding G-protein coupled receptor protein, GPR40, and clasmosis of diabetes, ketosis, acidosis, diabetic neuropathy, diabetic nephropathy, diabetic retinopathy, hyperlipaemia, skin diseases, conputatis, bone diseases, arteriosclerosis, thrombosis, hypertension, indigestion, memory loss, obesity, hypoglycaemia, edema, insulin allergy, fat metabolism disorders and cancer. This creatstance, insulin allergy, fat metabolism disorders and cancer. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LKAVEALASGAMPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                       antidiabetic, anabolic, neuroprotective; nephrotropic; ophthalmological; antidiabetic, dermatological; antiarteriosclerotic; antiarthritic; osteopathic; thrombolytic; nootropic; anorectic; hypotensive; cytostatic; diabetes; ketosis; acidosis; diabetic neuropathy; diabetic nephropathy; diabetic nephropathy; diabetic retinopathy; hyperlipaemia; skin disease; arthritis; memory loss; obesity; hypoglycaemia; edema; ingulin resistance; insulin allergy; fat metabolism disorder; cancer; hamster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MALSPQLEPALYVSAFALGFPLNLIAIRGAVARARIRLTPNLVYTLHLACSDLLLAITLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid and eicosanoid-binding G-protein coupled receptor prote:
GPR40 for control of pancreatic function and treatment of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Okubo S;
Fukusumi S;
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                                                                                                                        fatty acid; eicosanoid-binding G-protein coupled receptor;
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81.8%; Score 1295; DB 7; Length 3:
Best Local Similarity 80.7%; Pred. No. 1.1e-120;
Matches 242; Conservative 21; Mismatches 37; Indels
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Harada M, F
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Kawamata Y, Ogi K, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 245-246; 257pp; Japanese.
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12-NOV-2002; 2002JP-00328696.
22-JAN-2003; 2003JP-00014032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2003; 2003WO-JP001483
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                                       04-DEC-2003 (first entry)
                                                                                  Hamster GPR40 protein
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ADB61428 standard; protein; 300 AA

RESULT 12 ADB61428 ID ADB61-XX

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VKAVEALASGAWPLPLPLCPVFVLVHFAPLYAGGGFLAALSAGRYLGAAFPFGYQAVRRP 120
                                                                                     NASNVASFLYPNIGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
                                                                                                GPR 42; G-protein coupled receptor 42; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; syndrome x; antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; therapy.
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                                                             CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG
                                                    PARPSLSLLLPPLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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                                                                                                                                                                                                       Human G-protein coupled receptor GPR 42
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/label= Transmembrane
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/label= Transmembrane
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                                                                                                                                                  AAB82759 standard; protein; 346 AA
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22-MAR-2000; 2000GB-00007015.
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/label= Tr
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receptor useful for
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                                                                                                                                                                                                                                                                                      Homo sapiens
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                  121
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The present sequence is that of human G-protein coupled receptor 42 (GPR 42). The invention is based on the finding that expression of GPR 42 and

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GPR 41 (see AAB82758) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting lipplysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 activity, involving: (1) contacting a test agent with GPR 41 or GPR 42 or a variant polypeptide capable of coupling to a G-protein; and (2) monitoring for GPR 41 or GPR 42 activity in the presence of a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41 or GPR 42, an inhibitor of lipolysis, or a polynucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dyalipidaemia, coronary heart disease, atherosclerosis, thrombosis or obesity, angina, chronic metabolic syndrome (syndrome X) (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DLLLLLEIPPRAVEAANGMHWPLPFILCPLSGFIPFTTIYLTALFLAAVSIERFLSVAHP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVC- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 LEAWDP--ASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDTGPDQSYPSGNHWFVFSVYLLTPLVGLPLNLLALVVFVGKLRCRPVAVDVLLLNLTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 ALLTLLLCVGPYNASNVASFLYPNLGGS--WRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 TLINFLVCFGPYNVSHVVGYI---CGESPVWRIYVTLLSTLNSCVDPFVYYFSSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                  Length 346;
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Matches 101; Conservative 38; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                  23.1%; Score 366; DB 4; 34.1%; Pred. No. 6.8e-28;
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N-PSDB; AAA30762.
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Best Local S
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Homo sapiens.

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY906677 and AAY90677). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in IM6 to form a sequence X-C (AA)15-Pro. The endogenous proline in IM6 to form a sequence X-Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous candonists, agonists and partial agonists for use as pharmaceutical agenists. The mutant proteins are also useful in research settings for antagonists for a particular GPCRs are useful for treating diseases and disadrers associated with that receptors in normal and diseases and disadrers associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous Ingands. The present sequence the new and particular GPCR referred to in an exemplification of
Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                 Example 1; Page 310-311; 341pp; English.
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                                                               agents.
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## 24; Gaps 21.9%; Score 347; DB 3; Length 346; 32.3%; Pred. No. 5.4e-26; ive 41; Mismatches 134; Indels 5 Query Match Best Local Similarity 32.3 Matches 95; Conservative Sequence 346 AA;

52 DLLLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111 61 DILILILELPERMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120 1.12 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171 172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228 : : | | : | | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 51 9 1 MDTGPDQSYFSGNHWFVFSVYLLITFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS 1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS 230 TLLNFLVCFGPYNVSHVVGYICGE-SPAMRIYVTLLSTLNSCVDPFVYYFSSSG 282 229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282 셤 ઠે a δ 셤 ઠે a ò 셤

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Human G-protein coupled receptor GPR 41.
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RESULT 15
                                                                                                 AAB82758
110 AAB8
120 AAB8
120
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GPR 41; G-protein coupled receptor 41; human; drug screening; dyslipidaemia; coronary heart disease; atherosclerosis; thrombosis; obesity; angina; kidney failure; peripheral vascular disease; stroke; diabetes; metabolic syndrome; syndrome x, antilipaemic; cardiant; antiatherosclerotic; thrombolytic; anorectic; antianginal; nephrotropic; vasotropic; cerebroprotective; antidiabetic; therapy.

Identification of an agent for the modulation of G-protein coupled receptor useful for the treatment of disease i.e. dyslipidemia or stoke. .8. .41 /label= Transmembrane 229. .250 /label= Transmembrane 52. .73 /label= Transmembrane Transmembrane Transmembrane Transmembrane /label= Transmembrane Location/Qualifiers Claim 7; Page 44-46; 53pp; English. 19-FEB-2001; 2001WO-GB000684. 18-FEB-2000; 2000GB-00003900. 22-MAR-2000; 2000GB-00007015. 188. .212 /label= Tr .153 88. .111 /label= T label= (GLAX ) GLAXO GROUP LTD. WPI; 2001-536581/59. Wise A, Brown AJ; N-PSDB; AAH26459 WO200161359-A2 23-AUG-2001 Domain Domain Domain Domain Domain Domain Domain 

The present sequence is that of human G-protein coupled receptor 41 (GPR 41). The invention is based on the finding that expression of GPR 41 and C GPR 42 (see ABB82759) is restricted to adipose tissue. GPR 41 or GPR 42 may therefore be used as a screening target for the identification and development of novel pharmaceutical agents for use in inhibiting and the comparis. Methods are claimed for identifying agents that modulate GPR 11polysis. Methods are claimed for identifying agents that modulate GPR 41 or GPR 42 or a variant polypeptide capable of coupling to a G-protein, and (2) monitoring for GPR 41 or GPR 42 activity in the presence of a G-protein, thereby determining whether the test agent modulates activity. Such agents, which may be an activator of GPR 41, GPR 42, an inhibitor of lipolysis, or a polynucleotide encoding GPR 41, GPR 42 or variant polypeptide, are useful for the treatment of dyslipidaemia, coronary heart disease, atherosclerosis, thrombosis or obesity, angina, chronic renal failure, peripheral vascular disease, stroke, type II diabetes or metabolic syndrome (syndrome X) (all claimed)

Sequence 346 AA;

9 1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS 24; Gaps Length 346; 21.9%; Score 347; DB 4; Length 34(32.3%; Pred. No. 5.4e-26; ive 41; Mismatches 134; Indele Local Similarity 32.3 nes 95; Conservative Query Match Matches

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DILLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111 ||||| : || : ||| || ||| ||| ||| ||| DILILILIPIPERMVERANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120 52

112 IGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171 .. ---

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Db 121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIBFSGD-ISHSQGTNG-----TCY 170

Qy 172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCTVGCLRALARSGLTHRRKLRAAWVAGG 228
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5055	_	RLVWILGRGG-S
2		SLVWI)
7	<del>-</del>	YCYSI
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414		FWP
	::	EMAVVI
25.5	_	LLPVRI
2		BFRKDQLAILLPVRLE
10 DE		LEFR
7		171

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230 TLLNFLVCFGFYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDFFY

Search completed: April 29, 2004, 12:10:03 Job time : 61 secs

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OM protein - protein search, using sw model

April 29, 2004, 12:07:54 ; Search time 20 Seconds (without alignments) 1442.873 Million cell updates/sec Run on:

US-10-202-687-2 1584 Title: Perfect score:

1 MDLPPQLSFGLYVAAFALGF......RGPGLKTVCAARTQGGKSQK 300 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI .	Description
1	1584	100.0	300	7	JC5714	G protein-coupled
7	366	23.1	346	7	JC5716	
m	347	21.9	346	7	JC5715	G protein-coupled
4	332	21.0	330	7	JC5717	G protein-coupled
ເດ	244	15.4	420	7	151667	thrombin receptor
9	228	14.4	425	7	A37912	thrombin receptor
7	213	13.4	427	7	S17148	alpha-thrombin rec
8	205.5	13.0	363	7	I57940	somatostatin recep
σ	204.5	12.9	355	~	JQ1231	interleukin-8 rece
10	204	12.9	432	~	A43448	thrombin receptor
11	201	12.7	358	~	A53752	interleukin-8 rece
12	198.5	12.5	328	~	JC4800	P2Y6 receptor - hu
13	197.5	12.5	328	~	I55450	G protein-coupled
14	195.5	12.3	362	~	868207	G protein-coupled
15	194.5		350	7	A39445	interleukin-8 rece
16	194	12.2	363	7	I57955	somatostatin recep
17	194		364	~	JN0763	somatostatin recep
18	190.5		354	~	153033	G protein-coupled
19	190.5		362	~	A57641	
20	189.5		359	~	JC5277	G protein-coupled
21	188.5	11.9	352	٦	S27357	
22	186.5		362	~	B57641	G protein-coupled
23	186	11.7	375	~	A54946	P-2U nucleotide re
24	184	11.6	365	N	868679	G protein-coupled
25	$\sim$	11.5	355	~	149339	macrophage inflamm
56	182.5	11.5	360	~	A53611	interleukin-8 rece
27	180.5	11.4	355	~	A45177	chemokine (C-C) re
28	179	11.3	373	N	A47556	ATP receptor P2u -
29	179	11.3	384	~	A47249	brain-specific som

G protein-coupled	G procein-coupled	kappa opioid recep	opioid receptor ho	G_protein-coupled	G protein-coupled	G protein-coupled	bradykinin Bl_rece	heptahelical P2Y5-	interleukin-8 rece	delta opioid recep	G protein-coupled	somatostatin recep	G protein-coupled	intron 17 purinerg
B45680	JN0605	149022	JC2421	156520	S68208	150241	S60024	JC5549	S42096	B48227	S32785	JC4629	G02064	T09508
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361	388	367	367	367	365	308	352	370	356	372	374	384	360	344
11.2	11.2	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.7
178	175.5	173.5	173.5	173.5	173	172.5	172	172	171.5	171.5	171.5	171	170.5	169.5
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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ESG	C5714	

RESULT 1

UC5714
G protein-coupled receptor 40 - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1997 #sequence\_revision 23-Jan-1998 #text\_change 21-Jul-2000
C;Accession: UC5714
R;Sawadargo, M.; George, S.R.; Nguyen, T.; Xu, S.; Kolakowski Jr., L.P.; O'Dowd, B.F.
B;Sawadargo, M.; George, S.R.; Nguyen, T.; Xu, S.; Kolakowski Jr., L.P.; O'Dowd, B.F.
A;Accession: UC5714
A;Accession: UC5714
A;Accession: UC5714
A;Residues number: UC5714
A;Residues number: UC5714
A;Residues: L-300 c-SAM>
A;Acsion: UC5714
A;Residues: L-300 c-SAM>
A;Acsion: Doc SAM>
A;Acsion: Domain: Lransmembrane #status predicted crMu>
F;13-32/Domain: transmembrane #status predicted crMu>
F;13-144/Domain: transmembrane #status predicted crMu>
F;184-20C,Domain: transmembrane #status predicted crMu>
F;185-144/Domain: transmembrane #status predicted crMu>
F;262-243/Domain: transmembrane #status predicted crMu>
F;265/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;289/Binding site: palmitate (Cys) (covalent) #status predicted

0; Gaps Length 300; 0; Indels DB 2; 100.0%; Score 1584; DB 2; 100.0%; Pred. No. 2.8e-125; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 300; Conservative

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9 1 MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTFSLVYALNIGGSDLLLTVSLP 1 MDLPPQLSFGLYVAAFALGPPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP g ð

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120 9 61 LKAVEALASGAWPLPASLCPVPAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP ઠે

61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120 셤

180 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 121 ò 셤

240 240 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY PARFSLSLLIFFLDLAITAFCYVGCLRALARSGLTHRRKKIRAMWAGGALLTLLLCVGPY 181 181 ò 셤

241 NASNVASFLYPNIGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300 ઠે

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95; Conservative
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Best Local Similarity
Matches 95; Conserv
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JUESTIES

G protesin-coupled receptor 41 - human

C;Species Homo sapiens (man)

C;Species Homo sapiens (man)

C;Species Homo sapiens (man)

C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 29-Sep-1999

C;Accession: JCS715

S;Sawadargo, M; George S.R.; Nguyen, T; Xu, S; Kolakowski Jr., L.F.; O'Dowd, B.F.

Biochem. Biophys. Res. Commun. 239, 543-547, 1997

A;Title: A cluster of four novel human G protein-coupled receptor genes occurring in clc

A;Reference number: JCS714; MUID:98008875; PMID:9344866

A;Accession: JCS715

A;Accession: JCS715

A;Accession: JCS715

A;Molecule type: MRNA
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A;Accession: UC5714; MUID: 98008875; PMID: 9344866
A;Accession: UC5716
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Superfamily: G protein-coupled receptor 43
C;Keywords: 91ycoprotein
F;18-41/Domain: transmembrane #status predicted <TM1>
F;52-73/Domain: transmembrane #status predicted <TM2>
protein-coupled receptor 42 - human species Homo sapiens (man) protein-coupled receptor 42 - human species Homo sapiens (man) spaces 30 - Boc-1997 #sequence_revision 03-Dec-1997 #text_change 29-Sep-1999 Accession: 0C5716 Accession: 0C5716 Accession: Nguyen, T.; Zu, S.; Kolakowski Jr., L.F.; O'Dowd, B.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 LEAWDP--ASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DILLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
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A, Cross-references: GB: AF024688; NID: 92612947; PIDN: AAB86711.1; PID: 92612948
C, Superfamily: G protein-coupled receptor 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
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F;130-153/Domain: transmembrane #status predicted <TM5>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;220-250/Domain: transmembrane #status predicted <TM6>
F;259-278/Domain: transmembrane #status predicted <TM7>
F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 366; DB 2
Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.1%;
34.1%;
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Best Local Similarity
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G protein-coupled receptor 43 - human G protein-coupled receptor 43 - human G species: Homo aspiens (man) C species: Homo C 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DILLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SISITLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDLPPQLS-----FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 ILLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;86-105/Domain: transmembrane #status predicted <TW3>
F;128-147/Domain: transmembrane #status predicted <TW4>
F;128-204/Domain: transmembrane #status predicted <TW5>
F;20-242/Domain: transmembrane #status predicted <TW6>
F;256-276/Domain: transmembrane #status predicted <TW7>
F;151,167/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG
                                                                                                                                                                                                                                                                                                                                                                            24;
F;229-250/Domain: transmembrane #status predicted <TW6>
$1.559-278/Domain: transmembrane #status predicted TTW7-
F;166/Binding site: carbohydrate #status predicted
F;295/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 21.0%; Score 332; DB 2; Length 33:
Local Similarity 31.0%; Pred. No. 2e-20;
hes 93; Conservative 53; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches 134; Indels
                                                                                                                                                                                                                                                                   21.9%; Score 347; DB 2; 32.3%; Pred. No. 1.2e-21;
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C;Accession: S11148
R;Rasmussen, U.B.; Vouret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavirani, PEBS Lett. 288, 123-128, 1991
A;Fitle: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca(; A;Reference number: S17148; MUID:91348247; PMID:1652467
                                                                                                               269 YYFSA-----FSAVFFFVPLIISTVCYVSIIRCLSSSAVANRSKKSRALFLSAAVFCIF 322
                                                                                                                                                                                                                                                                                                                                                                                                       227 WALAIA--GVVPLVLKEQTIQVPG-----LINITI-----CHDVLNETLLEGYYA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 DWQFGSGMCRFATAAFYCNMYASIMLMTVISIDRFLAVVYPIQSLSWRTLGRANFTCLVI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 WVWAI--MGVVPLLLKEQTTRVPG-----LNITT-----CHDVLNETLLQGFYS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 YYFSA-----FSAVFELVPLISTICYMSIIRCLSSSSVANRSKKSRALFLSAAVFCVF 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solution teceptor 5 - rat somatoatain receptor 8. Tat NyAlternate names: somatotropin release-inhibiting factor subtype 28 receptor Cispecies: Ratus norvegicus (Norway rat) Cibate: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Nov-1999 R;0'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-thrombin receptor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                         11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                        167 DWQFGSBLCRFVTAAFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
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                                                                                                                                                                                                                                                                                                                                           131 WALVLCHLGLV-----FGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA-----
          42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X61958; NID:g940495; PIDN:CAA43957.1; PID:g49538
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.4%; Score 213; DB 2; Length 42
Best Local Similarity 23.4%; Pred. No. 2.4e-10;
Matches 68; Conservative 53; Mismatches 122; Indels
          46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 LLCVGPYNASNVASFLY 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IICFGPTNVLLIAHYSF 339
      65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <RAS>
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      Matches
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                                                                                                                                                                                                                                                                                                                                                         Cipemoin Interprof. Antican clawed frog)
Cipemoin Interprof. Aftican clawed frog)
Cipedoin 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipate: 17-Sep-1996
RiGeraten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
A;Reference number: IS1667; MUID:94195429; PMID:8145852
A;Accession: IS1667
A;Accession: IS1667
A;Accession: IS1667
A;Accession: London Company A;Reference manhalated from GB/EMBL/DDBJ
A;Residues: 1-420 cGER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A;Title: Molecular cloning of a functional thrombin receptor reveals a novel proteolytic
A;Reference number: A37912; MUID:91168254; PMID:1672265
182 ELCLVLPFIPMAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVTLLNPLVCFGPYN 239
                                                                                                        295
                                                                                                                                           240 VSHLVGY-HQRKSPWWRSIAVVPSSLNASLDPLLPYFSSSVVRRAFGRGLQVL---RNQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 DWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRPLAVVYPMHSLSWRTMSRAYMACSFI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYTVVPIVGLPLALLAIIIFLFKMKVR-KPAVVYMLALAIADVFFVSVLPFKIAYHLSGN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSP-----VCLEAWDPASAGPARF- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 WLISIA------STIPLLVTEGTQKIPRLDITTCHDVLDLKDLKDFYIY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 ---SLSILILFFLPIAITAFCYVGCLRALARSGLTHR-RKIRAAWVAGGALLTILLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 YFSSFCLLFFFVPFIITTICXIGIIRSLSSSSIENSCKKTRALFLAVVVLCVFIICFGPT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLPLKAVEALASG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5q13-5q13
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
P;1-26/Domain: signal sequence #status predicted <SIG>
P;27-425/Product: thrombin receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombin receptor precursor - human
C;Specise: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C;Accession: A37912
                                                                                                 242 ASNVASFLYPNLGGSWRKLGLITGAMSVVLNPLVTGYLGR-----GPGLKTVCAARTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g495198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 N-----ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%; Score 228; DB 2; Length 425; 25.3%; Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 4.1.,
25.0%; Pred. No. 6e-13;
rive 44; Mismatches 126; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GDB:127737; OMIM:187930
                                                                                                                                                                                                                                                                  RESULT 5
151667
thrombin receptor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 25.09
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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A; Residues: 1-425 < VUA>
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Length 355;

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C;Accession: A43448

Z;Zhong C.; Hayzer, D.J.; Corenon, M.A.; Runge, M.S.
J; Biol. Chem. 267, 16975-16979, 1992

A;Title: Molecular cloning of the rat vascular smooth muscle thrombin receptor. Evidence A;Title: Molecular at NUID:92381002; PMID:1324917

A;Accession: A43448

A;Status: preliminary
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
J. Immunol. 148, 1261-1264, 1992
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor. A;Reference number: A46483; MUID:92148149; PMID:1737938
A;Recession: A46483
A;Recession: A6483
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <LEE>
A;Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Residues: aneutrophils
A;Reperimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: Vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VVIYALVFLESLIGNSLVMLVILYSRSNRSVTDVYLLNLAMADLLFALTMPIMAVS--KE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 IWALSLI-LSLPFFLFRQ------VFSPNNSSPVC---YEDLGHNTAKWRWVLR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ASNVASFLYPNLGGSWRKIJGLITGAWSVVLN 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 KGWIFGTPLCKVVSLVKEVNFYSGILLLACISVDRYLAIVHATRTLTQKRHLVKF-ICLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 IWALVICHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 L-----FFLPLAITAFCYVGCLRAL--ARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 ILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGOKH----RAMRVIFAVVLIFLLCWLPYN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombin receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VAAFALGFPLNVLA---IRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LYVAAFALGFPLNVLAIRGATAHARLRL-TPSLVYALNLGCSDLLLTVSLPLKAVEALAS
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Local Similarity 24.5%; Pred. No. 1.4e-09;
nes 63; Conservative 46; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.9%; Score 204.5; DB 2; Length : 1 Similarity 25.8%; Pred. No. 1e-09; 83; Conservative 39; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 LVLLADTLMRTHVIQETCQRRNDIDRALDATEILGFLHS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIIYAFIGONFRNGFLKMLAAR 328
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Matches 63;
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Best Local S:
Matches 83
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                                                                                                                                                                                                                                   A;Residues: 1-363 <OCAL>
A;Cross-references: GB:L04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R;C'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref A;Reference number: IS7949; MUID:94088493; PMID:8264565
                            A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: 157940; MUID:93125499; PMID:1362243
A;Accession: 157940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 AWPLPASLCPVF----AVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;MOJecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 341-363 <0CA2>
A;Cross-references: GB:867370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental source: pituitary
A;Experimental source: pituitary
B;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the mucleotide and amino acid sequence of th
A;Reference number: 839244
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                                                                                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: SSTR5
C, Superfamily: vertebrate rhodopsin
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Description-coupled P2 receptor - rat
Classical Rattus norregicus (Norway rat)
Classical Rattus norregicus (Norway rat)
Classical Sattus norregicus (Norway rat)
Classical Sattus norregicus (Norway rat)
Classical Sattus Paracesical Sattus Sa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLG---YQAFRR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 PCYSWGVCAAIWALVL--CHLGLVPGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 A--AWLVCVAVWLAVTTQCLPTAIF------AATGIQ---RNRTVCYDLSPPA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 SAG---PARFSLSLLLFFLPLAITAFCYVGCLRA--LARSG-----LTHRRKLRAMVAG 227
                                                                                                                                                              A.Reference number: H01373
A.Recension: G02544
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 'M',4-328 <HAM>
A.Kresidues: 'M',4-328 <HAM>
C.Genetics: COM CBL TON: ARBO3572.1; PID:g1407633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 LPP----VYSAVLAAGLPLNICVIT-QICTSRRALTRTAVYTLNLALADLLYACSLPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 GALLTLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 VVAAAFAISFLPFHITKTA-----YLAVRSTPGVPCTVLEAFAAAYKGTRP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P;104-122/Domain: transmembrane #status predicted <TVM3>
P;143-167/Domain: transmembrane #status predicted <TVM4>
P;193-216/Domain: transmembrane #status predicted <TVM5>
P;241-264/Domain: transmembrane #status predicted <TVM6>
P;283-305/Domain: transmembrane #status predicted <TVM7>
P;283-305/Domain: transmembrane #status predicted <TVM7>
P;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: glycoprotein; placenta; receptor; transmembrane protein F;26-52/Domain: transmembrane #status predicted <TWM1> F;63-86/Domain: transmembrane #status predicted <TWM2>
A;Cross-references: EMBL:X97058
A;Experimental source: placenta
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 12.5%; Score 197.5; DB 2; Local Similarity 26.2%; Pred. No. 3.7e-09; nes 77; Conservative 30; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: P2Y6
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-8 receptor (clone 5Bla) - rabbit (Species: Oryctolagus cuniculus (domestic rabbit) (Species: Oryctolagus cuniculus (domestic rabbit) (Species: Oryctolagus cuniculus (domestic rabbit) (Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (Spacesion: A53752 R.P., Suzuki, H.; LaRosa, G.N.; Wilkinson, N.; Folco, E.; Navarro J. Biol. Chem. 269, 12391-12394, 1994 (Spacesion: Affitle: Modecular characterization of a novel rabbit interleukin-8 receptor isotype. A;Reference number: A53752; MUID: 94230294; PMID: 8175642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricommuni, D.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept A;Reference number: JC4800; MUID:96222498; PMID:8670200
A;Accession: JC4800
A;Molecule type: mRNA
                                                                                                                                                                                                                                                            275 SYYFSA-----FSAIPFLVPLIISTVCYTSIIRCLSSSAVANRSKKSRALFLSAAVFCI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 ---PPNSSPVCYEDMGNSTA-KWRWVLRILPQIFGFILPLLVWLFCYVFTLRTLFQAHMG 242
                                                                                              233 IWVMAI--MGVVPLLLKEQTTQVPG-----LNITT-----CHDVLNETLLHGFY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINIGCSDLLLTVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 INLAIADILIPATTLPIWAASKV--HGWTFGTPLCKVVSLVKEVNPYSGILLLACISVDRY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 LGAAFPLGYQAFRRP----CYS-WGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 LAIVHATRIMOKRHLVKFICLSMWGVSLILSLPILLFRNAIF-------- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 QKH----RAMRVIFAVVLIPLICWLPYNLVLLTDTLMRTHVIQETCERRNDIDRALDATE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 DLPPTLLDSAPCRSESLETNSYVVLITYILVFLLSLIGNSLVMLVILYSRSTCSVTDVYL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLPP------QLSFGLYVA--AFALGFPLNVLA---IRGATAHARLRLTPSLVYA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
Accession: JC4800; G02514
                                                                                                                                                                                                  ---SAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 INTPVNGSPVCLEAWDPASAGPARFSLSLLL----PFLPLAITAFCYVGCLRAL--ARSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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IWALVICHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.7%; Score 201; DB 2; Length 358;
Best Local Similarity 25.5%; Pred. No. 2e-09;
Matches 89; Conservative 34; Mismatches 122; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 VASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR--GPGLKTVCAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CLNPIIYAFIGOKFRYGLLKILAA 329
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                                                                                                                                                                                                                                                                                                                                                                                                     233 LLLCVGPYNASNVASFL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 PIVCFGPTNVLLIVHYL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 ILGFLHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
JC4800
P2Y6 receptor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A53752
                                                                                                                                                                                                  178
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12;

51;

82

10;

Gaps

47;

IndelB

Matches

62

3 LPPOLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK

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A; Molecule type: DNA
A; Residues: 1-350 <RES>
A; Residues: 1-350 <RES>
A; Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047
B; Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A; Title: Comparison of the genomic organization and promoter function for human interleub A; Reference number: 137898; MUID:95014476; PMID:7929358
A; Reference number: 137898; MUID:95014476; PMID:7929358
A; Residues: 1-350 <RE2>
A; Ross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A; Ross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
A; Residues: 1-16 <RE3>
A; Residues: 1-16 <RE3>
A; Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
B; Holmes, W.E.; Lee, J.; Kanag, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A; Title: Structure and functional expression of a human interleukin-8 receptor.
A; Ross-reference number: A39445; MUID:91369199; PMID:1840701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 NGWIFCTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHATRTLTQKRHLVKF-VCLG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 CWGLSM-NLSLPPFLFRQA-----YHPNNSSPVCYEVLGNDTA-KWRMVLRIL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L----FFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNASNV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 PHTFGFIVPLEVMLFCYGFTLRTLFKAHM--GQKHRAMRVIFAVVLIFLLCWLPYNLVLL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 IWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VAAFALGFPLNVLA---IRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A39445
A;Molecule type: mRNA
A;Residues: 1-275, Tr, 277-350 <HOL>
A;Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C;Genetics:
A;Gene: GDB:IL8RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: GDB:135039, OMIM:146929
A, Map Dostition: 2435-2435
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 ADTLMRTQVIQESCERRNNIG---RALDATEILGFLHSCLNPIIYAFIGQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 ASFLY------PNLGGSWRKLGL--ITGAWSVVLNPLVTGYLGR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%; Score 194.5; DB 2; 28.3%; Pred. No. 7e-09; iive 39; Mismatches 126;
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nes 82; Conservative
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Best Local S:
Matches 82,
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C,Accession: 137449; 138710; 138711; A39445
C;Accession: 137449; 138710; 138711; A39445
E;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A,Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 regi
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PEBS Lett. 375, 121-124, 1995

A,Title: Cloning, sequencing and tissue distribution of two related G protein-coupled A,Reference number: S68207; MUID:96087098; PMID:7498459
A,Accession: S68207
A,Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                  120 PCYSWGVCAAIWALVL--CHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA 177
                                                                                                                                                                                                                    -----AATGIQ---RNRTVCYDLSPPI 184
                                                                                                                                                                                                                                                                              SAG---PARFSLSLLLFFLPLAITAFCYVGCLRALARSG-----LTHRRKLRAAWVAGGA 229
                                                                                                                                                                                                                                                                                                                 185 LSTRYLPYGMALTVIGFLLPFTALLACYCRMARRICRQDGPAGFVAQERRSKAARMAVVV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 WGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV------ 169
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                                                    AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLG---YQAFRR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYS 123
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A;Cross-references: BMBL:U35399; NID:g1015420; PIDN:AAA79061.1; PID:g1015421
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
S68207
G protein-coupled receptor 6C.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S68207
R;An, S.; Tsai, C. Coor-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 PP----SLYIFVIGVGLPTNCLALMAAYRQVQQR-NELGVYLLNLSIADLLYICSLPLWV
29 LPP-----VYSVVLVVGLPLNVCVIAQICA-SRRTLTRSAVYTLNLALADLLYACSLPLL
                                                                                                     83 IYNYARGDHWPFGDLACRLVRFLFYANLHGSILFLTCISFORYLGICHPLAPWHKRGGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAVFVISFLPFHITKTA-----YLAVRSTPGVSCPVLETFAAAYKGTRP 288
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Best Local Similarity 27.2%; Pred. No. 5.9e-09;
Matches 74; Conservative 30; Mismatches 115; Indels 53
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N;Alternate names: interleukin-8 receptor, high-affinity
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                     :|| :| :| || 1143 A--AWVVCGVVWLVVTAQCLPTAVF-
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11;

43;

Length 350; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

April 29, 2004, 12:11:34 ; Search time 47 Seconds (without alignments) 1769.295 Million cell updates/sec

1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300 US-10-202-687-2 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1138120 seqs, 277189581 residues Searched:

1138120 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database

(gm2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
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(cgm2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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(cgm2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	250, App	475, App	33080, A	2, Appli	272, App	4, Appli	254, App	605, App	2, Appli	33898, A	274, App	2, Appli	4, Appli	258, App	467, App
Description	Sequence	Sequence		Sequence			Sequence	Sequence		Sequence	Sequence		Sequence	Sequence	Sequence
ΔI	US-10-251-385-250	US-10-225-567A-475	US-10-029-386-33080	US-10-202-687-2	US-10-251-385-272	US-10-203-539-4	US-10-251-385-254	US-10-225-567A-605	US-10-203-539-2	US-10-029-386-33898	US-10-251-385-274	US-10-348-190-2	US-10-348-190-4	US-10-251-385-258	US-10-225-567A-467
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* Nery Match Length DB	300	300	300	300	300	346	346	346	346	401	346	330	330	330	330
Query Match	100.0	100.0	100.0	100.0	7.66	23.1	21.9	21.9	21.9	21.9	21.6	21.5	21.1	21.0	21.0
Score	1584	1584	1584	1584	1579	366	347	347	347	347	342	340.5	334	332	332
Result No.	-	7	٣	4	Ŋ	<b>.</b>	7	æ	σı	10	11	12	13	14	15

234, 1004, 1	2 2 4 4 4 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
14 US-10-337-992-2 14 US-10-029-386-34068 14 US-10-029-386-34068 19 US-09-852-161-104 9 US-09-852-659A-104 19 US-09-852-79-104 10 US-10-081-810-41 12 US-10-081-810-43 12 US-10-081-810-43 14 US-10-255-567A-516 14 US-10-255-567A-516 15 US-10-25-67A-516 16 US-10-25-67A-516 17 US-10-25-67A-516 18 US-10-25-67A-516 19 US-09-782-980-80 10 US-09-782-980-80 11 US-10-187-691-7 12 US-10-081-810-42 13 US-10-081-810-42 14 US-11-255-57A-324 15 US-10-1336-489-4	14 US-10-177-293-130 16 US-10-176-4264-3 16 US-10-431-224-5 16 US-10-431-234-11 14 US-10-251-385-186 12 US-10-400-991-1 14 US-10-190-469-1 15 US-10-173-151-2 16 US-09-739-151-2 10 US-09-782-974C-76 12 US-10-081-810-2
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11110222222222222222222222222222222222	W W W W W A A A A A A A A A A A A A A A

## ALIGNMENTS

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Sequence 250, Application US/10251385
| Publication No. US20030105292A1
| Publication No. US20030105292A1
| Publication No. US20030105292A1
| APPLICANT: Chalmers, Derek T. APPLICANT: Chalmers, Derek T. APPLICANT: Chalmers, Derek T. TITLE OF INVENTION: Receptors
| TITLE OF INVENTION: Receptors | TITLE OF INVENTION: Receptors | FILE REFERENCE: AREN-0040 |
| CURRENT APPLICATION NUMBER: US/10/251,385 |
| CURRENT APPLICATION NUMBER: US/09/170,496 |
| PRIOR APPLICATION NUMBER: US/09/170,496 |
| PRIOR APPLICATION NUMBER: US/09/170,496 |
| PRIOR PELING DATE: 1998-10-13 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO S: 294 |
| SEQ ID NO SEQ ID NO SEGO ID NO S
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Best Local Similarity 100.
Matches 300; Conservative
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CORGANISM: Homo sapiens
US-10-251-385-250
JS-10-251-385-250
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61 LKAVBALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120

121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180

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US-10-202-687-2
; Sequence 2, Application US/10202687
; Publication No. US20040019109A1
; GENERAL INFORMATION:
; APPLICANT: OLDE, BJORN
; APPLICANT: OLDE, BJORN
; APPLICANT: FLOGREN, REIK
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS AFFECTING FATTY ACID
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS AFFECTING FATTY ACID
; TITLE OF INVENTION: METHODS.
; CURRENT FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 4
; CURRENT FILING DATE: 2002-07-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                                                                                                                                                         Length 300;
               SEQ ID NO 33080

LENGTH: 300

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: MAP TO U62631.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: WISSPROT HIT: O14842, EVALUE 0.00e+00

US-10-029-386-33080
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                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1584; DB 14; Best Local Similarity 100.0%; Pred. No. 4.4e-139; Matches 300; Conservative 0; Mismatches 0;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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LENGIH: 300
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                                                                                                                                                                                                                                                                                                                            Sequence 475, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT PEPLING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
SHIOR PLING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin Version 3.1
SEQ ID NO 475
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Sublication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: HANZEL DAVID RENOWED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APLICATION NUMBER: US/10/12-20

NUMBER OF SEQ 1D NOS: 34288
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  121 CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
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                                                     PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
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CORGANISM: Homo sapiens
US-10-225-567A-475
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Best Local Similarity
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US-10-029-386-33080
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US-10-225-567A-475
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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Lidaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REPERSIVE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT APPLICATION NUMBER: US/10/251,385
PRIOR PILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-13
SOFTWARE: PATENTING DATE: 294
SOFTWARE: PATENTING NOS: 294
SOFTWARE: PATENTING NOS: 294
SOFTWARE: PATENTING NOS: 294
SOFTWARE: PATENTING NOS: 294
SOFTWARE: ALTHUR DATE: 1998-10-13
SEQ ID NO 254
LENGTH: 346
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Best Local Similarity 34.1%; Pred. No. 1.1e-25;
Matches 101; Conservative 38; Mismatches 129;
PRIOR APPLICATION NUMBER: GB 0007015.1
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 3.0
SEQ ID NO 4
LENGTH: 346
TYPE: PRT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human of TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REPERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                      241 NASNVASFLYPNIGGSWRKIGLITGAWSVVINPLVTGYLGRGPGIKTVCAARTQGGKSQK 300
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Pred. No. 1.3e-138;
0; Mismatches 1;
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; Publication No. US20030113810A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL ASSAY
; FILE REFERENCE: FG3849USw
; CURRENT APPLICATION NUMBER: US/10/203,539
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: GB 0003900.8
                                                                                                                                                                                                                                                                                                                                        Sequence 272, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 272
LENGTH: 300
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Best Local Similarity 99.7%;
Matches 299; Conservative
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; ORGANISM: Homo sapiens
US-10-251-385-272
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Best Local Similarity
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61 DILLILEEPERMYEAANGMHWPLPPILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95; Conservative
                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           i NAME/KEY: TRANSMEM
i LOCATION: (259)..(278)
US-10-203-539-2
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NAME/KEY: TRANSMEM
LOCATION: (18)..(41)
FEATURE:
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Best Local Similarity
Matches 95; Conserva
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                                                                                                                                                                                                                                                                           APPLICANT: LifeSpan Biosciences
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brumer, Gaena C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT FALING DATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
   ----TCY 170
                                    172 EAW---DPASAGPARFSLSLILFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                      61 DLLLLELPRRAVERANGMAMPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 IGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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                                                                                                                           230 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 282
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                                                                                                         229 ALLTLLLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.9%; Score 347; DB 14; Length 346; Best Local Similarity 32.3%; Pred. No. 6.6e-24; Matches 95; Conservative 41; Mismatches 134; Indels 24;
 121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIEFSGD-ISHSQGTNG--
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Publication No. US20030113810A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL ASSAY
FILE REFERENCE: PG3849USW
CURRENT APPLICATION NUMBER: US/10/203,539
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: GB 0003900.8
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-03-22
                                                                                                                                                                                                                            Sequence 605, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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US-10-225-567A-605
                                                                                                                                                                                                           US-10-225-567A-605
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LENGTH: 346
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US-10-203-539-2
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APPLICANT: Louahed, Jeanila
APPLICANT: Louahed, Jamila
APPLICANT: Louahed, Jamila
APPLICANT: Louahed, Jamila
APPLICANT: Levitt, Roy
APPLICANT: Levitt, Roy
APPLICANT: Dong, Qu
TITLE OF INVENTION: Atchma Associated Factors as Targets for Treating
FILE REFERENCE: 036870-5072
CURRENT PAPLICATION NUMBER: US/10/348,190
CURRENT PAPLICATION NUMBER: US/09/157,24
FRIOR FILING DATE: 1998-09-18
FRIOR FILING DATE: EARLIER FILING DATE: 1997-09-19
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/059,510
FRIOR PALING DATE: EARLIER FILING DATE: 1996-12-02
SPRIOR FILING DATE: EARLIER FILING DATE: 1996-12-02
SPRIOR FILING DATE: EARLIER FILING DATE: 1996-12-02
SOFTWARE: PATENTY FILING DATE: 1996-12-02
SOFTWARE: PATENTY FILING DATE: 1996-12-02
SEQ ID NOS: 27
LENGTH: 330
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171 LEFRKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGG-SHRRQRRVKGLLAA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 RWYLPKIVCALTGFGFYSSIYCSTWLLAGISMERYLGVAFPVQYKLSRRPLY--GVIAAL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 LSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNA
                                                                        230 TLINFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDFFVYYPSSG 282
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Publication No. US20030166150A1
GENERAL INFORMATION:
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Louahed, Jamila
APPLICANT: Levitt, Roy
                                                                                                                                                                                                                                                                                      Jean-Christophe
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                                                                                                                                                                                                              Sequence 2, Application US/10348190
Publication No. US20030166150A1
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Matches 99; Conservative
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ORGANISM: Murinae gen. 8p
US-10-348-190-2
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US-10-348-190-4
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Sequence 274, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Proctein-Coupled
TITLE OF INVENTION: Receptors
FILE REFREENCE: AREA 0040
CURRENT PILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/10/251,385
CURRENT PILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                              56 MDTGPDQSYFSGNHWFVFSVXLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAA 115
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                                                                                                                                      21.9%; Score 347; DB 14; Length 4 32.3%; Pred. No. 7.9e-24; ive 41; Mismatches 134; Indels
                 OTHER INFORMATION: MAP TO U62631.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: SWISSPROT HIT: 014843, EVALUE 0.00e+00
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Best Local Similarity 32.04
Matches 94; Conservative
                                                                                                                                                               Best Local Similarity 32.3<sup>3</sup>
Matches 95; Conservative
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CRGANISM: Homo sapiens
US-10-251-385-274
                                                                   ; OTHER INFORMATIC
US-10-029-386-33898
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FEATURE:
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Search completed: April 29, 2004, 12:17:26
Job time : 48 secs
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SOFTWARE: Patentin version 3.1
SEQ ID NO 467
LENGTH: 330
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; ORGANISM: Homo sapiens
US-10-225-567A-467
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Best Local S:
Matches 93,
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Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT PILING DATE: 1998-10-13
              APPLICANT: Dong, Qu
TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
TITLE OF INVENTION: Atopic Allergies Including Asthma and Related Disorders
FILE REFERENCE: 036970-5072
CURRENT TILING DATE: 2003-01-22
CURRENT FILING DATE: 1998-09-18
PRIOR PLILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: BARLIER APPLICATION NUMBER: 60/059,510
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-19
PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSLLLPFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
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                                                                                                                                                                                                                                                                                                                                                              21.1%; Score 334; DB 14; Length 330;
31.0%; Pred. No. 1e-22;
tive 53; Mismatches 120; Indels 34; Gaps
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31.0%; Pred. No. 1.6e-22;
ive 53; Mismatches 120; Indels 34;
Nicolaides, Nicholas
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SEQ ID NO 258
LENGTH: 330
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Best Local Similarity 31.0 Marches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
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                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-10-348-190-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-251-385-258
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Best Local Similarity
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US-10-251-385-258
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APPLICANT: LifeSpan Biosciences
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                              239
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12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 467, Application US/10225567A; Publication No. US20030113798A1; GENERAL INFORMATION:
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Sequence 250, App
Sequence 272, App
Sequence 2, Appli
Sequence 256, Appli
Sequence 276, Appli
Sequence 2, Appli
Sequence 220, Appli
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Sequence 220, Appl
Sequence 220, Appl
Sequence 220, App
Sequence 220, App
Sequence 3, Appli
Sequence 7, Appli
                                                                                       April 29, 2004, 12:08:54 ; Search time 23 Seconds (without alignments) 673.382 Million cell updates/sec
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1584
1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-170-496D-272

US-09-170-496D-254

US-09-248-715-2

US-09-248-715-2

US-09-170-496D-274

US-09-170-496D-274

US-09-170-496D-276

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US-09-170-130-2

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US-08-475-130-2

US-08-475-130-2

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US-08-475-130-2

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US-08-475-130-2

US-08-477-136-220

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                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score;
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	8 6 6	228	88 8 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4.4.4	425	000	US-08-742-440A-7 Se US-08-560-098A-57 Se US-08-767-003-13	Sequence 7, 1 Sequence 57,	7, Appli 57, Appl		
	2 4 6	228	44.	. 4. 4	425				220, App		
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	36 37	228	5 14	4. 4.	425 358			Sequence 7, 1 Sequence 186,	7, Appli 186, App		
	38	216.5	13		358	4 6	US-09-170-496D-40 Se	Sequence 40,	Appl Appli		
	40	213	11	. 4.	358	m		Sequence 2, 1	2, Appli		
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	43	202	121		328	1 M	9		Appl		
	4.		17	φ,	328	m ·	-08-513-974B-380		380, App		
	4 7	202.5	77	<b>20</b>	328	4	US-09-461-436B-56 Se	sequence 56,	App1		
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	0/T-60-8/	1064-1	25.00		11	0/0	0.00000				
•	Patent	80.0 80.0	555533	9	101	2	Sequence 230, Application 03/031/0430D Patent No. 6555339				
•	GENERAL INFORMATION	INFC	RMATI	NO							
•••	APPLICANT:	ANT:	APPLICANT: Behan, Dominic	, Dom		€ دن۵					
	APPLICANT:	ANT	Liaw,	Chen W	n W.	4					
•••	TITLE	99	OF INVENTION:	×	0. 65	5533	TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human	Activated 1		G Protein-C	-uje
	FILE R	OF IF	IIILE OF INVENTION: RECE FILE REFERENCE: AREN-0040	AREN-	Receptors	202	m				
•	CURREN	TT APE	PLICAT	NOI	UMBER	ŭ,	CURRENT APPLICATION NUMBER: US/09/170,496D				
•• ••	CURREN	T FII	CURRENT FILING DATE: NUMBER OF SEO ID NOS:	ATE: NOS:	1998-10-13 294	-10	-13				
•	SOPTWARE:		Patentin version	In ve	raion	3.1					
	SEQ ID NO	LENGTH: 300	2 2								
[	; TYPE: PRT ; ORGANISM: Homo	TYPE: PRT ORGANISM: Homo		sapiens	gu						
•	Query Match	latch			100	100.0%;	Score 1584; DB 4; Length	300;			
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a	à	н	MOLPP	OLSFG	LYVAA	PALC	MDLPPQLSFGLYVAAPALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP	receptritasi	09 d.		
Δ	q	7	MDLPP.		LY.	- PAIS	MDLPPQLSFGLYVAAFALGFPLAVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSL	LGCSDLLLTVSI	9 -4		
0	ઠે	61	LKAVE	ALASG	AWPLP	ASLC	LKAVEALASGAWPLPASLCPVPAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYOAFRRP	AAFPLGYOAFRE	3P 120		
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a	'n	181	PARFS	rerrr	PFLPL	AITA	PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY	GALLTLLLCVG	PY 240		
Ω	QD	181	PARFS1	CSLLL	PFLPL	AITA	PARFSLSILLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY	GALLTLLLCVG	   240		

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RESULT 2 US-09-170-496D-272 'Sequence 272, Application US/09170496D 'Patent No. 6555339

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56 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS 115
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                                                                                                                                                                                61 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
                                                   112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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                                                                                             121 LWYKTRPRLGQAGLVSVACWLLASAHCSVVYVIEFSGD-ISHSQGTNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bergama, Derk
APPLICANT: Bergama, Derk
APPLICANT: Ganesh, Sathe
APPLICANT: Ganesh, Sathe
APPLICANT: Mao, Joyce
TITLE OF INVENTION: CDNA CLONE HNEDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: 2
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
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MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SUSPTWARE: FastSEQ for Windows Version 2.0
SUSPTWARE: VESTEM: US/08/820,521
APPLICATION NUMBER: US/08/820,521
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08820521
Patent No. 5942416
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ATTORNEY/AGENT INFORMATION:
ANAME: Han, William T
REGISTRATION NUMBER: 34,344
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TELECOMMUNICATION INFORMATION
TELEPHONE: 610-270-4026
TELEPAX: 610-270-4026
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LENGTH: 401 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-820-521-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-MAR-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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US-09-170-496D-254
INFORMATION:
Patent No. 655539
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Deek T.
APPLICANT: Liaw, Chen W.
ITILE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-III REFERENCE: AREN-0040
ITILE OF INVENTION: NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: Patentin version 3.1
SEQID NOS: 294
SEQID NOS: 294
SEQID NOS: 294
          APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT FAPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 222
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CYSWGVCAAIWALVLCHIGLUFGLVFGLEAPGGWLDHSNITSLGINTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NASNVASFLYPNIGGSWRKIGLITGAWSVVINPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRGPGLKTVCAARTQGGKSQK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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32.3%; Pred. No. 1.1e-21;
tive 41; Mismatches 134; Indels 24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1579; DB 4;
Pred. No. 8.5e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%;
Best Local Similarity 99.7%;
Matches 299; Conservative (
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Best Local Similarity 32...
Best Local Similarity
Local Similarity
Local Similarity
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US-09-170-496D-254
                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-170-496D-272
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172 EAW----DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
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    116 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIPFTTIYLTALFLAAVSIERFLSVAHP 175
                                            112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
                                                                                 176 LWYKTRPRIGGAGLVSVACWILASAHCSVVYVIEFSGD-ISHSQGTNG-----TCY 225
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                                                                                                                                                                                                                229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                          285 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
ON NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 401;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEBALEDC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,715
FILING DATE: 09-Feb-1999
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.9%; Score 347; DB 3;
32.3%; Pred. No. 1.4e-21;
tive 41; Mismatches 134
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-248-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09248715
Patent No. 6277960
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERGSMA, DERK
SATHE, GANESH M.
FUETTERER, WENDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-407-0700
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Best Local Similarity 32.3
Matches 95; Conservative
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US-09-248-715-2
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                                                                      172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                      226 LEPRKDQLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWIIGRGG-SHRRQRRVAGLLAA 284
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                                            LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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                                                                                                                                                                                                                                        285 TLLNFLVCFGPYNVSHVVGYICGE-SPAWRIYVTLLSTLNSCVDPFVYYFSSSG 337
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                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09248715
Patent No. 6207800
GENERAL INFORMATION:
APPLICANT: BERGEMA, DERK
APPLICANT: FUETTERER, WENDY
APPLICANT: PUETTERER, WENDY
APPLICANT: MAO, JOYCE
TITLE OF INVENTION: CDNA CLONE HNPDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rainer & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.9%; Score 347; DB 3; Length 401; 32.3%; Pred. No. 1.4e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: FREESE FOR Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/248,715
FILING DATE: 09-FEB-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,521
FILING DATE: 19-MAR-1997
ATTORNEY-AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 401 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Valley Forge
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US-09-248-715-2
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74 RWYLPKIVCALIGEGEYSSIYCSTWILAGISMERYLGVAPPVQYKLSRRPLY--GVIAAL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 LCLVLFFVPMAVTIFCYWRFVWIMLTQPHVGAQRRR--RAVGLAVVTLLNFLVCFGPYNM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 YVAAFALGPPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                               47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08788750
Patent No. 5910430
GENERAL INFORMATION:
APPLICANT: Ellis, Catherine
APPLICANT: Bergsma, Derk
TITLE OF INVENTION: No. 5910430el G-Protein Coupled Receptor
TITLE OF INVENTION: (HTADX50)
                                                                                                                                                                                                                                                                                                                                   Length 330;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                Score 340.5; DB
Pred. No. 3.8e-21
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,750
CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CURRENT APPLICATION NUMBER: US/09/187,710A CURRENT FILING DATE: 1998-11-06 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GRGPGLKTVCAARTQGGKSQ 299
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REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                21.5%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            Query Match 21.5
Best Local Similarity 30.9
Matches 99; Conservative
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APPLICATION NUMBER:
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                                                                                                                                                                                                                            ; ORGANISM: HOMO SAPIENS
US-09-187-710-2
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                                                                                                                                                                   LENGTH: 330
TYPE: PRT
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
||||| : || : ||| ||| ||| ||| || || DLLLLLFLPRRAVEAANGMHWPLPFILCPLSGFIFFTIYLTALFLAAVSIERFLSVAHP 175
                                                                                                                                                            176 LWYKTRPRIGQAGLVSVACWILLASAHCSVVYVIÈFSGD-ISHSQGTNG-----TCY 225
                                                                                                                                                                                                                            172 EAW---DPASAGPARFSLSLILFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                       61 DLLLLEFPRAVEAANGMEMPLPFILCPLSGFIFFTTIVLTALFLAAVSIERFLSVAHP 120
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| Sequence 2, Application US/09187710A
| Patent No. 6180365 |
| GENERAL INFORMATION: | APPLICANT: LANE, PAMELA |
| APPLICANT: ELSHOURBAGY, NABIL |
| APPLICANT: ELSHOURBAGY, NABIL |
| APPLICANT: VAWTER, LISA |
| TITLE OF INVENTION: MOUSE 7-TRANSMEMBRANE RECEPTOR GPR43 |
| FILE REFERENCE: GP-70566
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US-09-170-496D-274
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Best Local Similarity
Matches 94; Conserv
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LENGTH: 346
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Sequence 276, Application US/09170496D

Sequence 276, Application US/09170496D

Patent No. 655339

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-C TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-C TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-C TITLE OF INVENTION: NO. 655339-Endogenous, Constitutively Activated Human G Protein-C CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 276

LENGTH: 330
                                                    182 ELCLVLFFIPWAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVTLLNFLVCFGFYN 239
                                                                                                                                                                                                             240 VSHLVGY-HQRKSPWWRSIAVVFSSLNASLDPLLFYFSSSVVRRAFGRGLQVL---RNQG 295
        185 SLSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                             242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR------GPGLKTVCAARTQG 295
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FILE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER PILING DATE: 1998-03-12
EARLIER FILING DATE: 1998-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER PLING DATE: 1997-03-14
EARLIER PLING DATE: 1997-03-14
EARLIER PLING DATE: 1997-03-14
EARLIER PLING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER PLING DATE: 1997-03-14
EARLIER PLING DATE: 1997-03-14
EARLIER PLING DATE: 1997-05-30
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Best Local Similarity 31.0
Matches 93; Conservative
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US-09-170-496D-276
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US-09-152-060-104
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ELCLVLPFIPWAVTIFCYWRFVWIMLSQPLVGAQRRR--RAVGLAVTLLNFLVCFGPYN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 VSHLVGY-HQRKSPWWRSIAVVFSSLNASLDPLLFYFSSSVVRRAFGRGLQVL---RNQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 --WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV-CLEAWDPASAG---PARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 SLSLLLFFLPLAITAFCY---VGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 RWYLPKVVCALTSFGFYSSIYCSTWLLAGISIERYLGVAFPVQYKLSRRPLY--GVIAAL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --WALVICHIGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV-CLEAWDPASAG---PARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 VAWVMSFGHCTIVIIVQ-----YLNTTEQVR---SGNEITCYENFTDNQLDVVLPVRL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 YIIFLTGLPANLLALRAFVGRIRQPQPAPVHILLISLTLADLLLLLLLPFKIIEAASNF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YVAAFALGFPLINVLAIRGATAHARL-RLTPSLVYALINLGCSDLLLTVSLPLKAVEALASG
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                                                                                                                                                                                                                                                                                                                                                                                                                               21.0%; Score 332; DB 2; Length 330; 31.0%; Pred. No. 2e-20; ive 53; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.0%; Score 332; DB 4; Length 330; 31.0%; Pred. No. 2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Mismatches 120; Indels
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                                                                                                                         ä
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 31.0.
Best Local Similarity 31.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93; Conservative
                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-170-496D-258
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Best Local Similarity
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US-09-170-496D-258
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MAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) LOCATION: (260)
) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 RWYLPKVVCALTSFGFYSSIYCSTWLLAGISIERYLGVAFPVQYKLSRRPLY--GVIAAL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 --WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV-CLEAWDPASAG---PARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (190)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.3%; Score 322; DB 4; Length 330; Best Local Similarity 31.0%; Pred. No. 1.4e-19; Matches 93; Conservative 50; Mismatches 123; Indels
EARLIER FILING DATE: 1997-05-30
FEARLIER PILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-05
EARLIER PILING DATE: 1997-06-05
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PARENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (181)
: INFORMATION: Xaa equals any of
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (181)
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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Sequence 2, Application US/09053866
Patent No. 6111075
GENERAL INFORMATION:
APPLICANT: Xu, Wenfeng
APPLICANT: Yee, David P.

US-09-053-866-2

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----VLCHLGLVFGLEAPGGWLDHSNTSLG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 KAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LPPQLSFGLYVAAFALGFPLNVLAIRG-ATAHARLRLTPSLVYALNLGCSDLLLTVSLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AAWVAGGALLTLLLCVGPYNAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.6%; Score 231.5; DB 3;
Best Local Similarity 24.9%; Pred. No. 7.3e-12;
Matches 88; Conservative 29; Mismatches 123;
              PROTEASE-ACTIVATED RECEPTOR PAR4 (ZCHEMR2)
                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
FILLING DATE:
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: PROTEBASE-ACTIVAT
TITLE OF INVENTION: PAR4 (ZCHEWR2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEBE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-479-130-2
; Sequence 2, Application US/09479130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Leith, Debra R
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
TELEPAX: 206-442-6678
TELEPAX:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 YSWGVCAAIWAL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                         CITY: Seattle STATE: WA
                                                                                                                                                                                                         USA
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Search completed: April 29, 2004, 12:12:39 Job time : 25 Becs
                                                                                                                                              Sequence 2, Application US/09472130A Patent No. 6473765 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                   JS-09-472-130A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 RIAYHLRGQRWPFGEAACRLATAALYGHMYGSVLLLAAVSLDRYLALVHPLRARALRGRR 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |----337
| IRLTAVVLASAVAFFVPSNLLLLHYSDPSPSAWGNLYGAYVPSLALSTLNSCVDF----337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
14.6%; Score 231.5; DB 4; Length 385;
Best Local Similarity 24.9%; Pred. No. 7.3e-12;
Matches 88; Conservative 29; Mismatches 123; Indels 113;
Patent No. 6436400

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yee, David A
APPLICANT: Yee, David C
APPLICANT: Yee, David C
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
TITLE OF INVENTION: PRAR4 (ZCHEMR2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: PastESE for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/479,130 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSER: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98-10
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 YSWGVCAAIWAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-442-6678
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Leith, Debra K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WA COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SHWQPAFT-----CLALLGCFLPLLAMLLCYGATLHTLAASGRRYGHA
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APPLICANT: Xu, Wenfeng
APPLICANT: Presnell, Scott R.
APPLICANT: Yee, David P.
APPLICANT: Yee, Donald C.
APPLICANT: FOSter, Donald C.
TITLE OF INVENTION: PROTEASE ACTIVATED RECEPTOR PAR4
TITLE OF INVENTION: (ZCHEMR2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 98-10D2
CURRENT APPLICATION NUMBER: US/09/472,130A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/053,866
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FREESEG for Windows Version 3.0
SEQ ID NO 2
LENGTH: 385
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April 29, 2004, 12:07:24; Search time 45 Seconds (without alignments) 2103.455 Million cell updates/sec
                                                                                                                                                                US-10-202-687-2
1584
1 MDLPPQLSFGLYVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
i: sp_mammal:*
i: sp_mhc:*
i: sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8k3t5 mus musculu	Q8k3t4 rattus norv	Q8vck6 mus musculu	Q8bz77 mus musculu	Q86vz1 homo sapien	Q8n580 homo sapien	Q8jj23 oncorhynchu	Q8bud0 mus musculu	Q8mi04 ovis aries	Q7tmv7 mus musculu	Q9wu09 rattus norv	Q8n5s7 homo sapien	Q8byc4 mus musculu	Q7z3w3 homo sapien	Q8bjb7 mus musculu	Q7tle7 oncorhynchu
SUMMARIES	ID	Q8K3T5	Q8K3T4	Q8VCK6	Q8BZ77	Q86VZ1	Q8N580	08JJ23	QBBUDO	Q8MI 04	Q7TMV7	Q9WU09	Q8N5S7	Q8BYC4	Q7Z3W3	Q8BJB7	Q7T1B7
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STRAIN=BALB/C;
SITAIN=BALB/C;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF539809; AAN03478.1; -.
GO; GO:001584; P:indegral to membrane; IEA.
GO; GO:001584; P:indegral to coupled receptor activity; IEA.
GO; GO:000186; P:c-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR\_Rhodpsn.
InterPro; IPR0037; GPCRRHODPSN.
PRINTS; PR00337; GPCRRHODPSN.
PROSITE; PS50262; G PROTEIN\_RECEP\_F1\_2; 1.
SEQUENCE 300 AA; 31837 MW; AFF180F1686F8C17 CRC64;

SEQUENCE FROM N.A.

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Gapa

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Query Match 83.9%; Score 1329; DB 11; Length 300; Best Local Similarity 82.7%; Pred. No. 4.2e-99; Matches 248; Conservative 17; Mismatches 35; Indels 0

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	194.5	12.3	350	4	QBN6T6	_	sapien
19	on .	12.2	353	::	035797		rattus norv
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21	193	12.2	385	1:	090K40	Q9JK40 mus	mus musculu
23	191	12.1	377	13	07T2S9		carassius a
24	190	12.0	390	13	Q8AXM7		carassius a
25	188		319	4	Q9Y2T6		homo sapien
56	188		355	9	Q8HZN7	Q8hzn7 goril	la gor
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	-OCT-2002	(TrEMBLrel		22.	Created)		
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_	Tadayyon M.;		1				
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Ellis C.E., Elshourbagy N.;
Ellis C.E., Elshourbagy N.;
Submitted CAG-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AP539810; AAN03479.1; -.
EMBL; AP539810; AAN03479.1; -.
EQ; GO:001584; F:nboqpsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PR00037; GPCR_Rhodpsn.
PRNNTS; PR00237; GPCR_HODPSN.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
SEQUENCE 300 AA; 31835 MW; 4E882AB259A5DD4F CRC64;
1 MDLPPQFSFALYVSAFALGFPINLLAIRGAVSHAKLRITPSLVYTLHLGCSDLLLAITLP
                                                                                                                                                                                                                                                                                                                                                                           181 PARLSPSILLFFLPLVITAFCYVGCLRALVRSGLSHKRKLRAAWVAGGALLTLLLCLGPY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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81.7%; Pred. No. 2.2e-98;
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Last sequence update)
Last annotation update)
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Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
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08K314
ID 08K314
AC 08K3'
AC 08K3'
AC 08K3'
DT 01-01
DE 08K3'
CO DT 01-01
CO DT 01-01
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STRAIN=C57BL/6J; TISSUB=Colon;

STRAIN=C57BL/6J; TISSUB=Colon;

STRAIN=C57BL/6J; TISSUB=Colon;

AM MEDLINE=2234683; PubMed=12466851;

The FANYOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of the mature 420:563-573(2002).

REMBL: BC019570; AAH13570.1; -...

BMBL: AR545043; AAO16236.1; -...

BMBL: AR545043; AAO16236.1; -...

BMBL: AR545043; AAO16236.1; -...

BMBL: AR545043; AAO16231 c.integral to membrane; IEA.

GO: GO:00016021; C:integral to membrane; IEA.

GO: GO:0001849; F:receptor activity; IEA.

GO: GO:000186; F:G-protein coupled receptor protein signalin. ..; IEA.

InterPro; IRR00276; GPCRRHODDPSN.

PROSITE; PRO0237; GPCRRHODDPSN.

PROSITE; PRO0237; GPCRRHODDPSN.

PROSITE; PRO0237; GPCRRHODPSN.

PROSITE; PROSITE; PRO0237; GPRINTENEREPF1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 AWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
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                                                         01-MRR-2002 (TrEMBLrel. 20, Created)
01-MRR-2002 (TrEMBLrel. 20, Last sequence update)
01-MRR-2003 (TrEMBLrel. 24, Last annotation update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to G protein-coupled receptor 43 (Orphan GPCR protein).
GPR43 OR LSSIG.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SL;
Senga T., Twamoto S., Yoshida T., Yokota T., Adachi K., Azuma E.,
Hamaguchi M., Iwamoto T.;
Hamaguchi M., Iwamoto T.;
"LSSIG is a novel murine leukocyte specific GPCR that is induced lithe activation of STAT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Colon;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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330 AA
PRELIMINARY;
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NCBI TaxID=9606;
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SEQUENCE 39
                                                                                                                                                                                                                                                                                                                                                                            and mouse
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XM MEDLINE=22354683; PubMed=12466851;
XM THE FANTOM COnsortium,
XM THE FANTOM COnsortium,
XM The RANTOM Consortium,
XM The RANTOM Consortium,
XM THE RANTOM Consortium,
XM THE RIKEN Genome Exploration Research Group Phase I & II Team;
XM THABLYSIS of the mouse transcriptome based on functional annotation of G0,770 full-length cDNAs.";
XM NGT 1263-573 (2002).
XM MGD; MGI:1298207; P2r13.
XM MGD; MGI:1298207; GPCR_Rhodpsn.
XM MGD; MGI:1298207; GPCR_Rhodpsn.
XM MGD; MGI:1298207; GPCRHHODPSN.
XM MGD; MGI:1298207; GPROTEIN RECEP F1 1; 1.
XM MGGITE; PSSO0237; GPROTEIN RECEP F1 2; 1.
XM MGGITE; PSSO0237; GPROTEIN RECEP F1 2; 1.
XM MGGITE; PSSO0237; GPROTEIN RECEP F1 2; 1.
  ----TGYL 279
                       241 SHLVGF-YLRQSPSWRVEAVVFSSLNASLDPLLFYFSSSVVRRAFGKGLLLIRNPASSML 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 LTTGLCLVAWLSAATLALPLTLHRQTFRLAGSDRWLCHDALPLTEQT-----SHWR 254
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                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 222.5; DB 11; Length 396; 31.1%; Pred. No. 5.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches 131; Indels
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                                                                                                                                                                               Last sequence update)
Last annotation update)
243 SNVASFLYPNLGGSWRKLGLITGAWSVVLNPLV--
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                                                                                                                                                                   Created)
                                                                          300 GRG-AKETVEGTKMDRGGSQ 318
                                                  GRGPGLKTVCAARTQGGKSQ 299
                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                       Protease-activated receptor
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hes 88; Conservative
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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*** REDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shackinguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Storiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Abnes S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SLSLLLFFLPLAITAFCYVGCLRALARSGLTHRR--KLRAAWVAGGALLTLLLCVGPYN-
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40635 MW; 565C43660B3C0CF7 CRC64;
              24, Last sequence update)
25, Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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PRINTS; PR00237; GPCRRHODOPSN.
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01-JUN-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein.
359 AA; 4
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mykiss).";

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of rainbow trout (Oncorhynchus
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 RPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 SPRXIFGICCTIWVLV-------WTG-----SIPIYSFHGKVEKYMCFH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 NMSDDTWSAKVFFPLEVFGFLLPMGIMGFC---CSRSI--HILLGRRDHTQDWVQQKA-- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 IPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- DPASAGPARFSLSLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLR---LITPSLVYALNLGCSDLLLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SEQUENCE FROM N.A.
Kiryu I., Koellner B., Kuroda A., Ototake M., Dijkstra J.M.;
"A new probable G-protein coupled receptor gene associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor rhodopsinL-1.

G protein-coupled receptor rhodopsinL-1.

Encoupled mykiss (Rainbow trout) (Salmo gairdneri).

Eukaryota; Metagas; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC 451; GPR55.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007186; F:receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

InterPro; IPR000276; GPCR_Rhodpsn.

FFam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRH9DDSSN.

PROSITE; PS00237; GPCRH9DDSSN.

PROSITE; PS502262; G_PROTEIN RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Pancreas;
Straumberg R.;
Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032694; AAH32694.1; -.
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                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 209; DB 4;
Pred. No. 5.8e-09;
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                                                                      319 AA
                                                                                                                                                                                                                                                   Similar to G protein-coupled receptor 55.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 TLLLCVGPYNAS---NVASFLYPNLG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CIYSIAASLAVFVVSFLPVHLG 245
                                                                                                                                            Created)
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 27.4
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                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
SECUENCE
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                                                                                                       Q8N580;
                                                                      Q8N580
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                                                                                                       ACCOCCOS DITTERNATIONS SO OR SERVICE SO OR S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 ----LHKMQPNDNHTLCIESY-PSKEGFIIYRLITLSLSFIIPLAFIVILHRKTLRSLSA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 IGTLGTEERKHRIRGLLIL--LMVIFILVLGPYHITGCVKYIGLLLHGDACEWEKTVFVPY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 GGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDLPPQLSFG------LYVAAFALGFPLNVLAIRGATAHARLR 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 LIPS----LVYALINLGCSDLLLITVSLPLKAVEALASGAWPLPASLCPVFAVAHFFPLYAG 93
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases,
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001802; E:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR. Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; GFCRHODOPSN.
PROSITE; PS00237; GFRPEIN_RECEP_F11; 1.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; Bhodopsn.
Pfam; PF00001; 7tm_1; 1.
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
EMBL, AK085829; BAC39547.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 SNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSL--LLFFLPLAITAFCYVGCLR---A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARSGLTHRRKLRAAWVAGGALLTLLLCVGPYNASNVASFLYPNLGG---SWRK----
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                  DB 13; Length 343;
                                                                                                                                                                                                                                                                                                                                                                               55; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                    343 AA; 38830 MW; 761F06E57F76BB40 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Probable G protein-coupled receptor GPR4
                                                                                                                                                                                                                                                                                                                                  13.1%; Score 207; 23.7%; Pred. No. 9
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MEDLINE=22354683; PubMed=12466851;
The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 QLGRGLLSLNSVLDPILYTFL 297
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                                                                                                                                                                                                                                                                                                                                                                               76; Conservative
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Strausberg R.;
Submitted (MAY-2003) to the
EMBL; BC052868; AAH52868.1;
    367 AA;
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                                                                                                                                                                                                        76 VDYFLHHDNWIHGPGSCKLFGFIFYSNIYISIAFLCCISVDRYLAVAHPLRFARLRRVKT 135
                                                                                                                                                                                                                                                              136 AVAVSSVVWA-----TELG----ANSAPLFHDELFRDRYNHT 168
                                                                                                                                                                                                                                                                                         170 -CLEAWDPASAGPARFSLSLLL--FFLPLAITAFCYVGCLRALARSGLTHRR-KLRAAWV 225
                                                                                                                                                                                                                                                                                                                  169 FCFEKF-PMERWVÁWMLYRVFVGFLFPWALMLLCYRGILRÁVQSSVSTERQEKVKIKRL 227
                                                                                                                                        22 PP----SLYIFVIGVGLPTNCLAL--WAAYRQVRQHNELGVYLMMLSIADLLYICTLPLW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ41116; CAD29615.1; -.. GO; GO:0016021; C:integral to membrane; IRA. GO; GO:0004872; F:receptor activity; IRA. GO; GO:0004874; F:receptor activity; IRA. GO; GO:0001584; F:rhodopsin-like receptor activity; IRA. GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA. InterPro; IPR0001; Fra. 1; I. Affan; PP00001; Fra. 1; I. Affan; PP00001; Fra. 1; I. Affan; PP00001; GPCRHODOPSN. PROSITE; PS00237; GPCRHODOPSN. PROSITE; PS00237; GPROTEIN RECEP FI.1; 1.
                                                                                                                        4 PPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSL-VYALNLGCSDLLLTVSLPLK
                                                                                                Gaps
                                                                                                                                                                                                                                    123 SWGVCAAIWALVLCHLGLVPGLEAPGGWLDHSNTSLGINTPVNGSPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and tissue distribution of the ovine somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Debus N., Dutour A., Boudouresque F., Vuaroqueaux V., Oliver C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Debus N.; "Regulation of GH secretion in sheep: Role of somatostatin and
                                                                  Query Match
Best Local Similarity 27.5%; Pred. No. 1e-08;
Matches 75; Conservative 35; Mismatches 108; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Intercellular communications in Endocrinology University of Aix-Marseilles II, Marseilles, France.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOMATOSTATIN RECEPTOR SUBTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor subtype 5: osst5.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 365 AA; 41104 MW; 20D9P8128DE0EA37 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               226 AGGALLTLLLCVGPYNASNVA-SFLYPNLGGSW 257
                                                                                                                                                                                                                                                                                                                                                                228 ALSLIAIVLVCFAPYHALLLSRSAVY--LGRPW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatostatin receptor subtype 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Shaler N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Brownstein M., Soares M.B., Bonaldon M.F., Carninci P., Frange C.,

R. Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Guap L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

Nones S.J., Marra M.A.,

Rodersation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                           46 LYLLVCAVGLGGNALVIYVVLRHAKMK-TVTNIXILNLAVADVLLMLGLPFVATQN-AIS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                   104 YMPEGPVLCRLVMTLDGINQFTSIFC----LTVMSVDRYLAVVHPIRSARWRRPRVAKLA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 IIYTSVLGFFGPLLVICLCYVLIVVKLKASGVRVGSTRRRSERK--VTRMVVVVVLVFAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 CWLPFFIVNIVNLAFALPEEPASAGLYFFVVVLSYANSCA-NPCLYGFLSDNLRQSFRKV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 ---PYNASNVASFLY----PNLGGSWRKLGLITGAWSVVLNPLVTGYLG---RGPGLKT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 SAAVWAFSLVMSLPLVVFADIQEGW-----NT-----CNLTWPEPVGLWGAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 SL--SLLLFFLPLAITAFCYVGCLRALARSGL----THRRKLRAAWVAGGALLTLLLCVG
                                                                                                                                                                                                                               11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                   71 AWPLPASICPVF---AVAHFFPLYAGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 CAAIWAL-VLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAGPARF
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                       49;
                                                                           Length
                                                                                                                                                       Indels
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40269 MW; FA9CAB7AA8BBD764 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                       48; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
                                                                       DB 6;
                                                                           12.8%; Score 203.5; DB 6 26.9%; Pred. No. 1.8e-08;
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                               Ouery Match
Best Local Similarity 26.55
Best Local 84; Conservative
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Local Similarity
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QBN5S7
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                                                                                                                                                                                                                                                                               153 ILVFAQTLPLF-------LTPMSKEEGDKTTCMEY--PNFEGTASLPWI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LPLKAVBALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFR 118
                                                                                                                                                                                                                                                                                                                                                132 ALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVN----GSPVCLEAWDPASAGPAR---- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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                                                                                                                                                                                                                                                                                                                                                                                                                                        184 -FSLSLLLFFLPLAITAFCY--VGC--LRALARSGLTHRRKLRAAWVAGGALLTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DIPPOLSFGLYVAAFALGFPLNVLAIRGATA---HARLRLTPSLVYALNLGCSDLLLTVS
                                                                                                                                                         12 YVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sawzdargo M., Nguyen T., Lee D.K., Lynch K.R., Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.;
"Identification and cloning of three novel human G protein-coupled receptor genes GPR52, PSI-GPR53 and GPR55: GPR55 is extensively mol. Brain Res. 64:193-198(1999).

EMBL; AF100789; AAD22411.1;
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0016021; C:integral to membrane; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO:0007186; P:G-protein coupled receptor protein signalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6%; Score 199; DB 11; Length 29
25.8%; Pred. No. 3.4e-08;
ive 34; Mismatches 129; Indels
                                                            ; Score 200; DB 11; Length 35; Pred. No. 3.4e-08; 38; Mismatches 103; Indels
al protein.
357 AA; 40191 MW; 56B96775303FBDDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
34008 MW; 7D7A99596C21A030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99132385; PubMed=9931487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN
                                                                12.6%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| ||: :
248 VFILCFTPYHVA 259
                                                                                                              65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 -- LLCVGPYNAS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
296 2
296 AA;
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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Hypothetical
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09400
AC 09400
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
DE GPR5
GN RATTU
CC BUKAR
OC GO
DR 
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79 LPFKMILPQVKSSPSL--VFCTFVECLYFISMYGSVFTICFISLDRLLALQYPLLVNHFR 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 HALVSLA-VAPTFPPITTVTCYLLIRSL-RQGLRVEKRLKTKAVRMIAIVLAIFLVCFV 249
                                                                                            119 RPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINT---PVNGSPVCLEAWD 175
                                                                                                                                                                                                                      176 PASAGPARFSLSLLLFFLPLAITAFC---YVGCLRALARSGLTHRRKLRAAWVAGGALLT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LKAVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 PARFSLSLLLFFLPLAITAFCYVGCLRALARSGL--THRRKURAAWVAGGALLTLLLCVG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC031653; AAH31653.1; ...
GO; GO: 0016021; C:integral to membrane; IEA.
GO; GO: 0004872; F: receptor activity; IEA.
GO; GO: 0001869; F: receptor activity; IEA.
GO; GO: 0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IRRO0276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 SPRKTFGICCIIWMLV------WUG----SIPIYTFHRGVEGYKCFHNMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LYVAAFALGFPLNVLAIRGATAHARLRL-----TPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 198; DB 4; Length 33: 26.6%; Pred. No. 4.7e-08; tive 41; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA; 37860 MW; BBOCAFDOFC371D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
G protein-coupled receptor 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                233 LLLCVGPYNASNVASFLYPN 252
                                                                                                                                                                                                                                                                                                                                                                                                         FVVSFLPVHLGLFLQFLVRN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 PYHVNRSVYVLHYRSHGAS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYNASNVASFL-YPNLGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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62

122

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150 IAYHLNGNNWVFGEVLCRATTVIFYGNWYCSILLLACISINRYLAIVHPFTYRGLPKHTY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                         92 LSTKLIPAIYLLVFVVGVPANAVTL--WMLFFRTRSICTTVFYTNLAIADFLFCVTLFFK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 SWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLG--INTPVNGSPVCLEAWDPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ---ISLAFFGFLIPFVLIIYCYAAIIRTL--NAYDH----RWLMYVKASLLILVIFTICF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 ALVTCGLVWATVFLYMLPFFILKQBYYLVQPDITTCHDVHNTCESSSPFQLYYF---- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 PARFSLSLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLL---LCV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCY 122
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the FANTON CONSOLIUM,
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"Analysis of the mouse transcriptome based on functional annotation of
"Analysis of the mouse transcriptome based on functional annotation of
"Analysis of the mouse transcriptome based on functional annotation of
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"Analysis of 11-15-12-12"

EMBL, AK08944; BAC40886.1; -.

EMBL, AK08944; BAC40886.1; -.

EMBL, AK08944; EAC40886.1; -.

GO; GO:0001501; C:integric to membrane; IRA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:rhodopsin-like receptor protein signalin. .; IEA.

InterPro: PROMOUL; 7tm 1; 1.

PROSITE; PSSOL62; G PROTEIN RECEP FI 2; 1.

SEQUENCE 369 AA; 41696 MW; C8E68009710519EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GPYNASNV---ASFLYPNLGGSW--RKLGLITGAWSVVLNPLV-----TGYL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 APSNIILIIHHANYYYNNTDGLYFIYLIALCLGSLNSCLDPFLYFLMSKTRNHSTAYL 372
                                                                                                                                                                                                                                                                                                                                                                                                3 LPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNIGCSDLLLTVSLPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AVEALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCY
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                                                                                                                                                                                                                                                                                                                         38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Heubner D., Mewes H.W., Weil B., Amid C., Osanger
                                                                                                                                                                                                                                              Length 376;
                                                                                                                                                                                                                                              Query Match
12.5%; Score 198; DB 4; Length 37
Best Local Similarity 24.5%; Pred. No. 5.2e-08;
Matches 73; Conservative 42; Mismatches 145; Indels
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                             Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BS537386; CAD7628.1; -.
Hypothetical protein
SEQUENCE 376 AA; 42720 MW; 7638373C15A695DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.5%; Score 197.5; DB 11; 24.1%; Pred. No. 5.6e-08; iive 45; Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22354683; PubMed=12466851;
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hes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08BJB7
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Q8BJB7
SO DE RESTRESE DE LA PROPERCIONE DEL PROPERCIONE DE LA PROPERCIONE DEL PROPERCIONE DE LA PROPERCIONE D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AFP-----HULGYFLNMHCSILFLTCICVDRYLAIVQPEGSRRWRQPACAKAVCIFV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARFSLSLLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 WLAA----GVV-----FALTVLE 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 FLLPLLVISVFTGRIMCALSRPGLLRQGRQRRVRAMQLLLTVLVIFLVCFTPFHARQVAV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNa.";
Nature 420:563-573 (2002).
BEML; AK040547; BAC30623.1;
GO; OC1001541; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-procein coupled receptor protein signalin. .; IEA.
InterPro; IPR000776; GPCR_Rhodopsn.
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                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS00262; G PROTEIN RECEP F1_2; 1.
SEQUENCE 358 AA; 39431 MW; C6F7042ABDE9CA8F CRC64;
                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-OCT-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative G-protein coupled receptor homolog.
GPR20 OR A430106B11RIK.
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Last annotation update)
358 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Conservative
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PRELIMINARY;
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SEQUENCE PROM N.A.
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Q7Z3W3 RESULT 14 Q7Z3W3

148

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149 IAYHLNGNNWVFGEVTCRITTVVFYGNNYCAILILTCMGINRYLATAHPFTYQKLPKRSF 208
                                                                                                           234 L---LCVGPYNASNV---ASFLYPNLGGSW--RKLGLITGAWSVVLNPLV 275 : | | | : : | | | : : | | : 307 VIFTICFAPTNIILVIHHANYYYHNTNSLYFMYLIALCLGSLNSCLDPFL 356
                                                                                                                                                          Search completed: April 29, 2004, 12:11:31
Job time : 47 secs
         8 6 6 6 6 6
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OM protein - protein search, using sw model

Run on:

April 29, 2004, 12:04:08; Search time 18 Seconds (without alignments) 867.836 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-202-687-2 1584 1 MDLPPQLSFGLXVAAFALGF.....RGPGLKTVCAARTQGGKSQK 300

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	014442 homo sapien 015529 homo sapien 01552 homo sapien 01555 homo sapien 01555 homo sapien P47749 xenopus lae P47749 xenopus lae P56488 papie hamd 0996716 homo sapien 099678 homo sapien 099678 homo sapien 099678 mus musculu P30398 rattus norv P21109 cyctcolagus 09910394 rattus norv 097571 canis famil P2544 cycytcolagus 095771 canis famil P3544 cycytcolagus 097571 canis famil P26824 homo sapien 000554 homo sapien 000554 homo sapien 000554 homo sapien 0005675 mus musculu 0005675 mus musculu 0005678 mus musculu 092060 rattus norv P25024 homo sapien P55920 pan troglod P56012 rattus norv P55920 pan recollod P55920 pan recollod
SUMMARIES	GP40 HUMAN GP42 HUMAN GP43 HUMAN GP43 HUMAN PARI XEMIA PARI HUMAN PARI PAPHA GP92 HUMAN PARI CRILO P273 MELGA PARI CRILO PARI MOUSE P275 HUMAN P276 HUMAN P276 HUMAN P276 HUMAN P276 HUMAN P276 HUMAN P276 RAT PARI HUMAN PRARI RAT PILIBA RAT PILIBA RAT PILIBA PANTR PRARI PANTR
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Length	300 300 300 300 300 300 300 300
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Score	1584 1364 1366 1375 1375 1375 1375 1375 1386 1386 1386 1386 1386 1386 1386 1386
Result No.	

P30992 canis famil P41231 homo sapien P50132 cus scrofa C00270 homo sapien C28422 gorilla gor Q99296 homo sapien Q91js7 mus musculu P47748 cavia porce Q8807 pan troglod P51582 homo sapien Q9tuel oryctolagus
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                                                                                                                                                                                                                                                                                                             PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                                                                                                                                                                            181 PARFSLSLLIFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGGALLTLLLCVGPY
                                                                                                                                                                              MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
                                                                                                                                                        MDLPPQLSFGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLP
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Orphan receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Dowd B.F.;
As cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1.", Biochem. Biophys. Res. Commun. 239:543-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sawzdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.,
                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                               ;
0
                                                                                                    ; Score 1584; DB 1; Length 300;
; Pred. No. 9.7e-111;
0; Mismatches 0; Indels 0
                                                                   LINKED (GLCNAC. . .) (P. 77EF27DACD93E80B CRC64;
             6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable G protein-coupled receptor GPR42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 AA
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MEDLINE=98008875; Pubmed=9344866;
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                                                                            31457 MW;
                                                                                                     100.0%;
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15-JUL-1998 (Rel. 36, Last
28-FEB-2003 (Rel. 41, Last
                                                                                                                Best Local Similarity 100. Matches 300; Conservative
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198
222
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10 AA;
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015529;
 DOMAIN
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 LEAWDP--ASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                             MIM; 603822; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004330; F:G-protein coupled receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ALLTLLLCVGPYNASNVASFLYPNLGGS--WRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 TLLNFLVCFGPYNVSHVVGYI---CGESPVWRIYVTLLSTLNSCVDPFVYYFSSSG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%; Score 366; DB 1; Length 34 34.1%; Pred. No. 2.3e-20; tive 38; Mismatches 129; Indels
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1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL),
CYTOPLASMIC (POTENTIAL)
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03F6742DA4B798D0 CRC64;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Putative G protein-coupled receptor GPR41.
                                                                                                                                                                                               PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS002237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
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MEDLINE=98008875; PubMed=9344866;
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EMBL; AF024689; AAB86712.1;
EMBL; AC002511; AAB67885.1;
PIR; JC5716; JC5716.
Genew; HGNC:4500; GPR42.
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346 AA;
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                                                                                                                     TISSUE—CVARY,

WENDINEE-22388557; PubMed=12477932;

WA Strausberg R.D., Collins F.S., Wagner L.H., Derge J.G.,

Atlausner R.D., Collins F.S., Wagner L.H., Schaefer C.M., Schuler G.D.,

Atlachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Atlachako L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carminci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Blakesley R.W., Kraywinski M.I., Skalaka U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length

Thuman and mouse CDNA sequences.";

Thuman and mouse CDNA sequences.";

Thuman and mouse CDNA sequences.";

Thuman and mouse CDNA sequences.";
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-I- FUNCTION: Orphan receptor.
-I- SUBGELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                 "A cluster of four novel human G protein-coupled receptor genes occurring in close proximity to CD22 gene on chromosome 19q13.1."; Biochem. Biophys. Res. Commun. 239:543-547(1997).
Sawzdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.,
O'Dowd B.P.;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCRAC. . . ) (POTENTIAL)
B3B19D62D11B6BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 603821; -... Gintegral to plasma membrane; TAS. GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0004930; F:G-protein coupled receptor activity; TAS. GO; GO:0007186; P:G-protein coupled receptor protein signalin. InterPro; IPR00276; GPCR_Rhodpsn.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
1 EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC.
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38649 I
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PRINTS; PR00237; GPCRRHC
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                                                                                                                                                                                                                           61 DLLLLLFLPFRMVEAANGMHWPLPFILCPLSGFIFFTTIYLTALFLAAVSIERFLSVAHP 120
                                                                                                                                                                                                                                                                     112 LGYQAFRRPCYSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCL 171
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GO:0005887; C:integral to plasma membrane; TAS.
GO:0004930; F:G-protein coupled receptor activity; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
                                                                                                                                                                                 DLLLTVSLPLKAVBALASGAWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFP
                                                                                           1 MDLPPQLS------FGLYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCS
                                                                                                                                     1 MDTGPDQSYFSGNHWFVFSVYLLTFLVGLPLNLLALVVFVGKLQRRPVAVDVLLLNLTAS
                                                                                                                                                                                                                                                                                                                                                              172 EAW---DPASAGPARFSLSLLLFFLPLAITAFCYVGCLRALARSGLTHRRKLRAAWVAGG
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Lamerdin J.B., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 TLINFLVCFGPYNVSHVVGYICGE-SPAMRIYVTLLSTLNSCVDPFVYYFSSSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ALLTILLCVGPYNASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
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-i- SUBCELLUIAR LOCATION: Integral membrane protein.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98008875; PubMed-9344866;
Sawzdargo_M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.
                                              24;
    21.9%; Score 347; DB 1; Length 346; 32.3%; Pred. No. 6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                              41; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable G protein-coupled receptor GPR43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 AA
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Query Match
Best Local Similarity 32.3
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 VAWVMSFGHCTIVIIVQ-----YLNTTEQVR---SGNEITCYENFTDNQLDVVLPVRL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 RWYLPKVVCALTSFGFYSSIYCSTWLLAGISIBRYLGVAFPVQYKLSRRPLY--GVIAAL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 --WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPV-CLEAWDPASAG---PARF 184
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (FAR-1) (Thrombin receptor).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia, Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 ELCLVLFFIPMAVTIFCYWFVWIMLSQPLVGAQRRR--RAVGLAVVTLLNFLVCFGPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 YVAAFALGFPLNVLAIRGATAHARL-RLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ASNVASFLYPNLGGSWRKLGLITGAWSVVLNPLVTGYLGR-----GPGLKTVCAARTQG
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SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
GERSTEN R.B., Chen J., Ishii M., Ishii K., Nanevicz T.,
Turck C.W., Vu T.-K.H., Coughlin S.R.;
"Specificity of the thrombin receptor for agonist peptide is defined by its extracellular surface.";
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                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 332; DB 1; Length 330;
; Pred. No. 7.4e-18;
53; Mismatches 120; Indels
InterPro; lPRUCUL: 1.
PRINTS; PR00237; GERRHODOPSN.
PROSTTE; PR00237; G PROTEIN RECEP F1 1; 1.
PROSTTE; PS0262; GPROTEIN RECEP F1 2; 1.
G-procein coupled receptor; Transmembrane; Polymorphism.
1 12 EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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/FTId=VAR 011861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F4A8AC6AFBDF1E90 CRC64;
                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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nes 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA;
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 ---SLSLLLFFLPLAITAFCYVGCLRALARSGLTHR-RKLRAAWVAGGALLTLLLCVGPY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 YFSSFCLLFFFVPFIITTICYIGIIRSLSSSSIENSCKKTRALFLAVVVLCVFIICFGFT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 WALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSP-----VCLEAWDPASAGPARF- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 WLISIA------STIPLLVTEQTQXIPRLDITTCHDVLDLKDLKDFYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 DWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVYPMHSLSWRTMSRAYMACSFI
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coupled
                                                                  -1- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
K-A: LACK OF ACTIVATION BY THROMBIN.
D5163F56AFE12372 CRC64;
                                                                                                                                                                                                                                                                                                                                                  EMBL; U09632; AAA18498.1; -.
PIR; 151667; 151667.
InterPro; 1PR000276; GPCR Rhodpsn.
PROSTITS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Blood coagulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REMOVED FOR RECEPTOR ACTIVATION. PROTEINASE ACTIVATED RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
                      G proteins that stimulate phosphoinositide hydrolysis. SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 244; DB 1; Length 42; Pred. No. 3.1e-11; 44; Mismatches 126; Indels
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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25.0%;
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Best Local Similarity 25.0.
Best Total Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelets by thrombin.";
J. Clin. Invest. 103:879-887(1999).
-!-FUNCTION: Receptor for activated thrombin or trypsin coupled to G proteins that stimulate phosphoinositide hydrolysis. May play a role in platelets activation.
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- TRSUE SPECIFICITY: Widely expressed, with highest levels in lung, pancreas, thyroid, testis and small intestine. Not expressed in brain, kidney, spinal cord and peripheral blood leukocytes. Also detected in platelets.
PAR4 HUMAN STANDARD; PRT; 385 AA.
Q96RIO, 076067;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 4 precursor (PAR-4) (Thrombin receptor-like 3) (Coagulation factor II receptor-like 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Lymphoma; Whitmore 18465; WEDLINE=89281984; PubMed=9618465; Xu W.-F., Andersen H., Whitmore T.E., Presnell S.R., Yee D.P., Ching A., Gilbert T., Davie E.W., Foster D.C.; "Cloning and characterization of human protease-activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.L., Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
Coughlin S.R.,
"Protease-activated receptors 1 and 4 mediate activation of human
                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                              MEDLINE=98389762; PubMed=9722561;
Kahn M.L., Hammes S.R., Botka C., Coughlin S.R.;
"Gene and locus structure and chromosomal localization of the
procease-activated receptor gene family.";
J. Biol. Chem. 273:23290-23296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98379991; PubMed=9716134; Kahn M.L., Zheng Y.-W., Huang W., Bigornia V., Zeng D., Moff Farees R.V., Tam C., Coughlin S.R.; Had dual thrombin receptor system for platelet activation."; Nature 394:690-694(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS VAL-296 AND LEU-310. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel Nickerson D.A., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-47 AND ARG-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:6642-6646(1998).
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                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                    2RL3 OR PAR4
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337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 RIAYHLRGORWPFGEAACRLATAALYGHMYGSVLLLAAVSLDRYLALVHPLRARALRGRR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VLCHLGLVFGLEAPGGWLDHSNTSLG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------AMWAGGALLTLLCVGPYNAS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LPPOLSFGLYVAAFALGFPLNVLAIRG-ATAHARLRLTPSLVYALNLGCSDLLLTVSLPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 LRLTAVVLASAVAFFVPSNLLLLHYSDPSPSAWGNLYGAYVPSLALSTLNSCVDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.6%; Score 231.5; DB 1; Length 385;
24.9%; Pred. No. 2.4e-10;
tive 29; Mismatches 123; Indels 113; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 ----FIYYYVSAEFR------DKVRAGLFORSPGDTVASKASAEGG 373
                                      InterPro; IfR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS0262; G_PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
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CLEAVAGE (BY THROMBIN OR TRYPSIN)
                                                                                                                                                                                                                                                                                                                                                                           . .) (POTENTIAL)
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R->A: NO PROTEOLYTIC CLEAVAGE (BY
                                                                                                                                                    PROTEINASE ACTIVATED RECEPTOR 4.
                                                                                                                              REMOVED FOR RECEPTOR ACTIVATION
                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                               FTIG=VAR_012852
                                                                                                                                          (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                     POTENTIAL
                                                                                                  Blood coagulation; Polymorphism. SIGNAL 17
EMBL; AF055917; AAC25699.1; -. EMBL; AF384819; AAK61908.1; -.
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          EMBL; AF384819; AAK61908
Genew; HGNC:3540; F2RL3
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120
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385 AA;
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Best Local Similarity
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296
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                               602779;
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EMBL; AF080214; AAC28860.1; -.

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EMBL;
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"Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                    Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
                      PARI HUMAN STANDARD; PRT; 425 AA.
P25116; O96RF7; Q9BUN4;
01-MAY-1992 (Rel. 22, Created)
10-CT-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protetainase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
F2R OR PARI OR TR OR CF2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRATUM.
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
                                                                                                                                 AEQUENCE FROM N.A.
MEDLINE=91168254; PubMed=1672265;
Vu T.-K.H., Hung D.T., Wheaton V.I., Coughlin S.R.;
Molecular cloning of a functional thrombin receptor reveals a novel proteolytic mechanism of receptor activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDLINE=99318093; PubMed=10391209;
MEDLINE=99318093; PubMed=10391209;
Cargill M., Altehuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protease-activated receptors 1 and 4 mediate activation of human platelets by thrombin."; J. Clin. Invest. 103:879-887(1999).
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99178892; PubMed=10079109;
Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
Coughlin S.R.;
                                                                                                                                                                                                            Nickerson D.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Genet. 22:231-238(1999).
                                                                                                                                                                            Cell 64:1057-1068(1991).
                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of human genes."
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                 HUMAN
        RESULT 7
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                    Jander B.S.;
Janes B.S.;
Janes B.S.;
Nat. Ganet. 23:373-373(1999).

-I- FUNCTION: High affinity receptor for activated thrombin coupled to G proteins that stimulate phosphoinositide hydrolysis. May play a role in platelets activation and in vascular development.

role in platelets activation and in vascular development.
                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Platelets and vascular endothelial cells.
-!- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-!- PTM: Phosphorylated; probably mediating desenzitisation prior to the uncoupling and internalization of the receptor.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGO; GO: 0005794; C: Golgi apparatus; TAS.

RGO; GO: 0005887; C: integral to plasma membrane; TAS.

RGO; GO: 0005887; C: integral to plasma membrane; TAS.

RGO; GO: 0005102; F: receptor binding; TAS.

RGO; GO: 0005105; F: receptor binding; TAS.

RGO; GO: 0006919; P: caspase crivation; TAS.

RGO; GO: 0006928; P: ceal mediation; TAS.

RGO; GO: 000725; P: development; TAS.

RGO; GO: 0007125; P: development; TAS.

RGO; GO: 0007125; P: response to wounding; TAS.

RGO; GO: 0007125; P: response to wounding; TAS.

RGO; GO: 0007262; P: response to wounding; TAS.

RGO; GO: 0007262; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007262; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007260; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007260; P: STAT protein nuclear translocation; TAS.

RGO; GO: 0007260; P: RTAT protein nuclear translocation; TAS.

REPARE, PF00001; 7tm 1, 1.

RRINES; RRO0277; GPRRHODOPSN.
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PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Blood coagulation; Phosphorylation; Polymorphism; 3D-structure.
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMOVED FOR RECEPTOR ACTIVATION. PROTEINASE ACTIVATED RECEPTOR 1.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PDB; INRN; 31-MAY-94.
PDB; INRQ; 31-MAY-94.
PDB; INRR; 31-MAY-94.
Genew; HGNC:3537; F2R.
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                                                                                                                                                                                                                                                                                                                                                                   71 AWPLPASICPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCAAI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 YYFSA-----FSAVFFVPLIISTVCYVSIIRCLSSSAVANRSKKSRALFLSAAVFCIF 322
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15-JTL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTW: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Papio hamadryas (Hamadryas baboon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                       (POTENTIAL)
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A -> V (IN REF. 3; AAH02464).
C -> S (IN REF. 1).
41B742A99EEC96AB CRC64;
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                                                                                      N-LINKED (GLCNAC. . . ) (
N-LINKED (GLCNAC. . . ) (
S -> G (in dbSNP:5893).
/FTId=VAR 014167.
ASP/GLU-RICH (ACIDIC).
CLEAVAGE BY THROMBIN).
BY SIMILARITY.
N-LINKED (GLCNAC...) (
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1 Similarity 25.3%;
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NCBI_TaxID=9557;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable G protein-coupled receptor GPR92.
FORPS2 OR GPR93.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
EMBL; AF028727; AAB84191.1; -
HSSP; P34996; 1DDD.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                  REMOVED FOR RECEPTOR ACTIVATION. PROTEINASE ACTIVATED RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%; Score 226; DB 1; Length 425; 25.3%; Pred. No. 6.7e-10; Live 47; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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118FC5FB39D4DE2C CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL
ASP/GLU-RICH (ACIDIC).
CLEAVAGE (BY THROMBIN)
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N-LINKED (GLCNA,
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SECUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

BEDILINE-22040266, PubMed=12044878;

Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

"Identification of G protein-coupled receptor genes from the human
                                                                                                                                                                                                                         White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.; "Autosomal dominant hypophosphataemic rickets is associated with
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterProj IPR000276; GPCR_Rhodpsn.
Pfam; PR0001; Thm 1; 1.
PRINTS; PR00327; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                       MEDLINE=20517346; PubMed=11062477;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 26:345-348(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'EBS Lett. 520:97-101(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:13307; GPR92.
MIM; 606926; -.
                                                                                                                                                                                                                                                                                                                                                                              mutations in FGF23.";
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                                                                                                                                           SEQUENCE FROM N.A.
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                                                     NCBI_TaxID=9606;
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245 LCFVPYNSTLAVYGLLRSKLVAASVFARDRVRGVLAWWILLAGA-NCVLDPLVXYFSAEG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 YSWGVCAAIWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 RLLPLVLLABALGFLLPLAAVVYSSGRVFWTLARPDATOSORRRKTVRLLLAN--LVIFL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCVGPYNA----SNVASFLYP---NLGGSWRKLGLITGAWSVVLNPLVTGYLGRG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 RIHLVVYSLVLAAGLPINALALWVFLRALRVHSVVS-----VYMCNLAASDLIFTLSLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ---PARFSLSLLLFFLPLAITAFCYVGCLRALARSGLT---HRRKLRAAWVAGGALLTLL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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OYDOFLASHIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Mismatches 141; Indels
                   .protein coupled receptor; Transmembrane; Glycoprotein.
)MAIN 1 26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              -LINKED (GLCNAC. . .) (PC BA35709084BB6D84 CRC64;
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                         (POTENTIAL).
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29.1%; Pred. No. 2.6e-09;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-EBB-2003 (Rel. 41, Last annotation update)
Probable G protein-coupled receptor GPR20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 AA
                                                                                                                               3 (POTENTIAL)
CYTOPLASMIC (
G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                  4 (POTENTIAL)
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Gene 187:75-81(1997).
-1- FUNCTION: Orphan receptor.
                                                                                                                                                                                                                                                                                                                                                                             41346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 ----PGLKTVCAART 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 FRNTLRGLGTPHRART 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                           372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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 PROSITE; PS50262;
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Q99678;
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                            62 AIFLAGLVINGLALYVFCCRTRAK-TPSVIYTINLVVTDLLVGLSLPTRFAVYYGARGCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601908; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:000430; P:G-procein coupled receptor activity; TAS.
GO; GO:000430; P:G-procein coupled receptor protein signalin. ..; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PR000237; GPCRHODOPSN.
PROSITE; PS00237; GPRCHODOPSN.
PROSITE; PS50362; G-PROTEIN_RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 --AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGVCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 RCAFP-----HVLGYFLNMHCSILFLTCICVDRYLAIVRPEAPAACROPACARAVCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AIW----ALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SLSLLLFFLPLAITAFCYVGCLRALARSGLTH---RRKLRAAWVAGGALLTLLLCVGPYN 241
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUB SPECIFICITY: LIVER AND THE BRAIN REGIONS THALAMUS, PUTAMEN, AND CAUDATE, BUT NOT IN PRONTAL CORTEX, PONS AND HYPOTHALAMUS.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 AAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLK-AVEALASG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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N-LINKED (GLCNAC. .) (FOTENTIAL)
N-LINKED (GLCNAC. .) (FOTENTIAL)
258C663D455BIEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 216.5; DB 1; Length 358; 29.0%; Pred. No. 2.9e-09; Live 37; Mismatches 87; Indels 55
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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259 6
275 EX
296 7
296 7
16 N-
26 N-
38406 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 AA;
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PARI_CRILO
ID PARI_CRILO ST
AC Q00991, Q60461;
                                                                                                                                                                                                                                                                                                                                                                                  49
70
87
126
147
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DOMAIN
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SEQUENCE
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MIM; 60
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428 AA.

PRT;

STANDARD;

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01-APR-1993 (Rel. 25, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proteinase activated receptor 1 precursor (PAR-1) (Thrombin receptor)
                                                                                                                                                                                                                                                                                                          Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                       "CDNA cloning and expression of a hamster alpha-thrombin receptor coupled to Ca2+ mobilization."; FEBS Lett. 288:123-128(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S17148; P1746.
HSSP, P34996; 1DDD.
InterPro; IRR000276; GPCR_Rhodpsn.
PERM; P800001; 7rm 1; 1.
PRINTS; PR00237; GPRATHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS00262; GPROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Blood coagulation; P01morphism.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMOVED FOR RECEPTOR ACTIVATION (BY
                                                                                                                                                                 TISSUE-Lung;
MEDLINE-91346247; PubMed=1652467;
Rasmussen U.B., Vouret-Craviari V., Jallat S., Schlesinger Y., Pasmussen U.B., Vouret-Craviari V., Pouyssegur J., Pages G., Pavirani A., Lecocq J.P., Pouyssegur J., Obberghen-Schilling E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
POLY-SER.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
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                                                                                                                                                                                                                                                                                                  SEQUENCE OF 42-428 FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=10030;
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-!- FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP > ADP = UTP. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                       272 YYFSA-----FSAVFFLVPLIISTICYMSIIRCLSSSSVANRSKKSRALFLSAAVFCVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WALVLCHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPA----
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                                                                                                                                                                                                                                                                                                          11 LYVAAFALGFPLNVLAIRGATAHARLRLTPSLVYALNLGCSDLLLTVSLPLKAVEALASG
                                                                                                                                                                                                                                                                                                                                                                                              71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFFPLGYQAFRRPCYSWGVCAAI
(BY SIMILARITY)
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 LLCVGPYNASNVASFLYPNLGGSWRK-----LGLITGAWSVVLNPLVTGY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor)
P2RY3.
                                                                                                                                                                                                                      Length 428;
                                                                                                                                                                                                                                                               53; Mismatches 122; Indels
               CLEAVAGE (BY THROMBIN)
                                                                                                                                                                                                                      Score 213; DB 1;
Pred. No. 6.2e-09;
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                                                                                                                                                                                                                      13.4%;
23.4%;
                                                                                                                                                                                                                                                                 68; Conservative
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257
257
65
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262
384
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                                                                                                                                                                          428 AA;
                                                                                                                                                                                                                                          Similarity
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                    DISULFID
CARBOHYD
CARBOHYD
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                                                                                                                               VARIANT
                                                                                    CARBOHYD
                                                                                                           CARBOHYD
                                                                                                                                                                        SEQUENCE
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Best Local
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P2Y3 MELGA
AD 093361,
DT 16-0CT-
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InterPro; IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm\_1; 1.

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86 YWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHKKKGKKLTWLVCAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 IWALVLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAWDP---ASAGPARFSL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TORNRT-VCYDLSPPDRSASYFPYGITL 191
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DARI MOUSE

TO PARI MOUSE

TO 1-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DF 15-MAR-2004 (Rel. 43, Last annotation update)

TO REPROVE THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AWPLPASLCPVFAVAHFFPLYAGGGFLAALSAGRYLGAAFPL-GYQAFRRPCYSWGVCAA
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MEDLINE=96379236; PubMed=8784787;
Kahn M.L., 12hi K., Kuo W.L., Piper M., Connolly A., Shi Y.P.,
Kahn M.L., Lin C.C., Coughlin S.R.;
"Conserved structure and adjacent location of the thrombin receptor
and protease-activated receptor 2 genes define a protease-activated
mol. Med. 2:349-357(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 208; DB 1; Length 328; 30.3%; Pred. No. 1.2e-08; Live 25; Mismatches 105; Indels
                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2, 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN : 22 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Coughlin S.R.;
"Cloning of CDNA for the mouse thrombin receptor.";
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B74D49B99C7164A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 VWFIVIAQCLPTFVFASTG-----
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PRINTS; PR00237; GPCRRHODOPSN
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Matches 67; Conserv
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REVISIONS
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CONFLICT
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           DOMAIN
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ID SSR5 RAT
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    FRANSMEM
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                                                 'RANSMEM
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Matches
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Xue J., Jenkins N.A., Gilbert D.J., Copeland N.G., Sadler J.E.;
"Structure and localization of the thrombin receptor gene on mouse chromosome 13.";
Mamm. Genome 7:625-626(1996).
-!- FUNCTION: High affinity receptor for activated thrombin coupled G proteins that stimulate phosphoinositide hydrolysis.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: A proteolytic cleavage generates a new amino terminus that functions as a tethered ligand.
                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                            REMOVED FOR RECEPTOR ACTIVATION (B SIMILARITY).
PROTEINAGE ACTIVATED RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                      EMBL, 103529; AAA40438.1; -... EMBL, U36757; AAB38308.1; -... EMBL, U36756; AAB38308.1; -... EMBL, BC031516; AAB31516.1; -... EMBL, U55076; AAB00198.1; -... EMBL, U55076; AAB00198.1; -... EMBL, U55076; AAB00198.1; -... EMBL, U55076; AAB00198.1; JOINED. HSSP; P34996; 1DDD.
                                                                                                                                                                                                        STRAIN=129/Sv;
MEDLINE=96327649; Pubmed=8678993;
                                                                                                                                                                                                 SEQUENCE OF 1-74 FROM N.A.
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107
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1203
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171 TDWQFGSGMCRFATAAFYGNMYASIMLMTVISIDRFLAVVYPIQSLSWRTLGRANFTCVV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 IWALVLCHLGLVFGL-----EAPGGWLDHSNTSLGINTPVNGSPVCLEAWDPASAGPAR 183
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                          CLEAVAGE (BY THROMBIN) (BY SIMILARITY)
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                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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"Modecular cloning and expression of a pituitary somatostatin
receptor with preferential affinity for somatostatin-28.";
Mol. Pharmacol. 42:939-946 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                108; Indels
                                                                                                                                                                                                                                                                                    F -> S (IN REF. 1).
G -> Y (IN REF. 1).
R -> G (IN REF. 1).
V -> L (IN REF. 1).
S -> T (IN REF. 1).
395FD64FAE52C9BF CRC64;
                EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                              ASP/GLU-RICH (ACIDIC).
POLY-PRO.
                                                                                  B (FOIENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                            BY SIMILARITY.

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)

N-LINKED (GLCNAC. . .)
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01-FRE-1995 (Rel. 31, Last sequence update)
110-CTZ-2003 (Rel. 42, Last annotation update)
Somatostatin receptor type 5 (8S5R).
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                                                                          (POTENTIAL)
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MEDLINE=94195267; Pubmed=7908405;
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TISSUE-Pituitary;
MEDLINE-93125499; PubMed=1362243;
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                                                                                                                                                                                                                                                                                                                                                                    365 S
47790 MW;
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hes 64; Conservative
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430 AA;
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201 ITYTSVLGFFGPLLVICLCYLLIVVKVKAAGMRVGSSRRRRSBPKVTRMVVVVVLVFVGC 260
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PIR; JQ1231; JQ1231.

InterPro; IPROUGOT6; GPCR_Rhodpsn.
Pfam; PPO0001; 7tm 1; 1.

PRINTS; PRO0237; GPCRRHODOPSN.
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M82873; AAA31376.1;
                                                                  289 CAARTOG 295
                                                                                        320 CLRRGYG 326
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 AWPLPASLCPVF----AVAHFFPLYAGGGFLAALSAGRYLGAAFPLGYQAFRRPCYSWGV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 YWPFGSFLCRLVMTLDGINQFTSIFC----LMVMSVDRYLAVVHPLRSARWRRPRVAKMA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 CAAIWAL-VLCHLGLVFGLEAPGGWLDHSNTSLGINTPVNGSPVCLEAW-DPASAGPARF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SLSLLLFFLPLAITAFCYVGCLRALARSGL---THRRKLRAAWVAGGALLTLLLCVG- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 LYLLVCTVGLSGNTLVIYVVLRHAKMK-TVTNVYILNLAVADVLFMLGLPFLATQNAVVS 101
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Gaps
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                                                                                                             kidney, pancreas, cerebellum, or cortex. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 205.5; DB 1; Length 363; 25.4%; Pred. No. 1.9e-08; ive 49; Mismatches 135; Indels 45.
                                                                                                                                                                                                                                                                             Interproj IPRO00276; GPCR_Rhodpsn.
PEAM; PR00017, 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.

DOMAIN.

S EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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239 --PYNASNVASFLY----PNLGGSWRKLGLITGAWSVVLNPLVTGYLG---RGPGLKTV 288
                                             J. Immunol. 148:1261-1264(1992).

-I- FUNCTION: Receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. Binding of IL-8 to the receptor causes activation of neutrophils. This response is mediated via G-protein that activate a phosphatidylinositol-calcium second messenger system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Albino; TISSUE-Neutrophils;
MEDLINE=91056034; PubMed=1700779;
Thomas K.M., Pyun H.Y., Navarro J.;
"Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.";
J. Biol. Chem. 265:20061-20064 (1990).
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TISSUB SPECIFICITY: Neutrophils.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CAUTION: Was originally (Ref. 2) thought to be the receptor for fmet-Leu-Phe (N-formyl peptide receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91378994; PubMed=1898400; Beckmann M.P., Munger W.B., Kozlosky C., Vanden Bos T., Price V., Lyman S., Gerard N.P., Cerretti D.P.; Cerretti D.P.; "Molecular characterization of the interleukin-8 receptor."; Biochem. Biophys. Res. Commun. 179:784-789(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High affinity interleukin-8 receptor A (IL-8R A) (CXCR-1) IL8RA OR CXCR1.
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1168 RABIT
P21169.
01-FEB-1991 (Rel. 17, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
-^~~-2003 (Rel. 42, Last annotation updat
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48 VVIYALVFLISLIGNSLVMLVILYSRSNRSVTDVYLLIALAMADLLFALTMPIWAVS--KB 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 L-----FFLPLALTAFCYVGCLRAL--ARSGLTHRRKLRAAWVAGGALLTLLLCVGPYN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 ILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKH----RAMRVIFAVVLIFLLCWLPYN 264
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                                                                                                                                                                                                                                                                                               7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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PAFCPDHAYLGRLQGRRLDFR (IN REF. 2).
HA -> QS (IN REF. 2).
R -> C (IN REF. 2).
B -> EL (IN REF. 2).
FE49ACB9D1E0F21 CRC64;
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PROSITE; PS00237; G PROTBIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTBIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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287
355 AA;
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